



SspI

6358	TCATCAAAATATTAGCAGCATCCAGATTGGTTCAATCAACAAGGTACGAGCCATATC	6417
	AGTAGTTTTATAAATCGTCGTAGGICTAACCCAAAGTTAGTTGTTCCATGCTCGGTATAG	
	ACTTTATTCAAATTGGTATCGCCAAACCAAGAAGAACTCCCATCCTCAAAGGTTTGTA	6477
6418	TGAAATAAGTTTAACCATAGCGGTTTTGGTTCTTCCTTGAGGTTAGGAGTTTCCAAACAT	
	AGGAAGAATTCTCAGTCCAAGCCTCAACAAGGTCAGGGTACAGAGTCTCCAACCATTA	6537
6478	TCCTTCTTAAGAGTCAGGTTTCGGAGTTGTTCCAGTCCCATGTCTCAGAGGTTTGTAAT	
	GCCAAAAGCTACAGGAGATCAATGAAGAATCTTCAATCAAAGTAACTACTGTTCCAGCA	6597
6538	CGGTTTTCGATGTCCTCTAGTTACTTCTTAGAAGTTAGTTTTCATTGATGACAAGTCTGT	
	CATGCATCATGGTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGG	6657
6598	GTACGTAGTACCAGTCATTCAAAGTCTTTTCTGTAGGTGGCTTCTGAATTTCAATCACC	

FIG. 1A

6658 GCATCTTTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACCAGACAAAAA 6717
CGTAGAAACTTTTCATTAGAACAGTTGTAGCTCGTCGACCGAACACCCCTGGTCIGTTTTT
6718 AGGAATGGTGCAGAATTGTTAGGCGCACCTACCAAAGCATCTTTGCCCTTTATTGCAAAG 6777
TCCTTACCACGTCCTTAACAATCCGCGTGGATGGTTTTCTGTAGAAACGGAAATAACGTTTC
6838 ATAAAGCAGATTCCCTCTAGTACAAGTGGGGAACAAAAATAACGTGGAAAGAGCTGTCCTG 6897
TGTCGGGTGAGTGATTTACGCATACTGCTTGCGTCACTGCTGGTGTCTTCTTAAGGGAGAT
SspI
6898 TATAAGAAGGCATTCAATCCCATTTGAAGGATCATCAGATACTAACCAATATTTCTC 6954
ATATTCTCCGTAAGTAAGGTAACTTCCTAGTAGTCTATGATTGGTTATAAAGAG

FIG. 1B

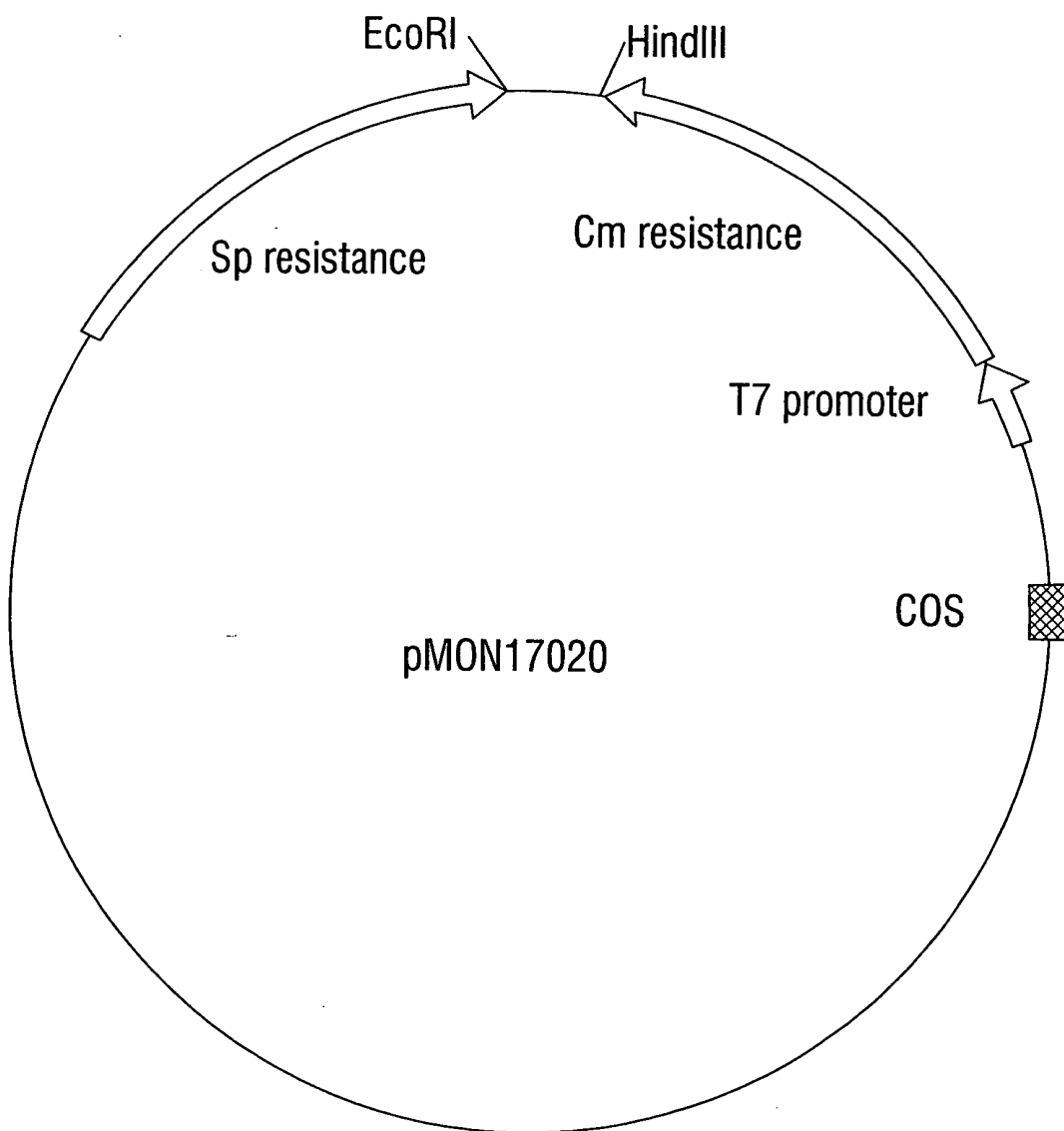


FIG. 2

FIG. 3A

FIG. 3B

CAG GGC TTT GGC GCC AAC CTT ACC GTC GAG ACG GAT GCG GAC GGC GTG Gln Gly Phe 210 Thr Val Glu Thr Asp Ala 220 Val	730
CGC ACC ATC CGC CTG GAA GGC CGC GGC AAG CTC ACC GGC CAA GTC ATC Arg Thr Ile Arg Leu Glu 225 Gly Lys Leu Thr Gly Gln Val Ile	778
GAC GTG CCG GGC GAC CCG TCC TCG ACG GCC TTC CCG CTG GTT GCG GCC Asp Val Pro Pro Asp 240 Ser Ser Thr Ala Phe 250 Val Ala Ala	826
CTG CTT GTT CCG GGC TCC GAC GTC ACC ATC CTC GTC CTG ATG AAC Leu Leu Val Pro Gly Ser 260 Ile Leu Asn Val Leu Met Asn	874
CCC ACC CGC ACC GGC CTC ATC CTG ACG CTG CAG GAA ATG GGC GCC GAC Pro Thr Arg Thr Gly 275 Thr Leu 280 Met Gly Ala Asp	922
ATC GAA GTC ATC AAG CCG CGC CTT GCC GGC GGC GAA GAC GTG GCG GAC Ile Glu Val Ile Asn Pro Arg 295 Leu Ala Gly Gly Asp Val Ala Asp	970
CTG CGC GTT CGC TCC TCC ACG CTG AAG GGC GTC ACG GTG CCG GAA GAC Leu Arg Val Arg Ser 310 Thr Leu Lys Gly Val Thr Val Pro Glu Asp	1018

FIG. 3C

CGC GCG CCT TCG ATG ATC GAC GAA TAT CCG ATT CTC GCT GTC GCC GCC	1066
Arg Ala Pro Ser Met Ile Asp Glu Tyr Pro Ile Leu Ala Val Ala Ala	320 325 330 335
GCC TTC GCG GAA GGG GCG ACC GTG ATG AAC GGT CTG GAA GAA CTC CGC	1114
Ala Phe Ala Glu Glu Gly Ala Thr Val Met Asn Gly Leu Glu Glu Leu Arg	340 345 350
GTC AAG GAA AGC GAC CGC CTC TCG GCC GGC AAT GGC CTC AAG CTC	1162
Val Lys Glu Ser Asp Arg Leu Ser Ala Val Ala Asn Gly Leu Lys Leu	355 360 365
AAT GGC GTG GAT TGC GAT GAG GGC GAG ACG TCG CTC GTC GTG CGC GGC	1210
Asn Gly Val Asp Cys Asp Glu Gly Glu Thr Ser Leu Val Val Arg Gly	370 375 380
CGC CCT GAC GGC AAG GGG CTC GGC AAC GCC TCG GGC GCC GTC GCC	1258
Arg Pro Asp Gly Lys Gly Leu Gly Asn Ala Ser Gly Ala Ala Val Ala	385 390 395
ACC CAT CTC GAT CAC CGC ATC GCC ATG AGC TTC CTC GTC ATG GGC CTC	1306
Thr His Leu Asp His Arg Ile Ala Met Ser Phe Leu Val Met Gly Leu	400 405 410 415
GTG TCG GAA AAC CCT GTC ACG GTG GAC GAT GCC ACG ATG ATC GCC ACG	1354
Val Ser Glu Asn Pro Val Thr Val Asp Asp Ala Thr Met Ile Ala Thr	420 425 430

FIG. 3D

```
AGC TTC CCG GAG TTC ATG GAC CTG ATG GCC GGG CTG GGC GCG AAG ATC 1402
Ser Phe Pro Glu Phe Met Asp Leu Met Ala Gly Leu Gly Ala Lys Ile
435 440 445
GAA CTC TCC GAT ACG AAG GCT GCC TGATGACCTT CACAATCGCC ATCGATGGTC 1456
Glu Leu Ser Asp Thr Lys Ala Ala
450 455
CCGCTGCGGC CGGCAAGGGG ACGCTCTCGC GCCGTATCGC GGAGGTCTAT GGCTTTTCATC 1516
ATCTCGATAC GGGCCTGACC TATCGCGCCA CGGCCAAAGC GCTGCTCGAT CGCGGCCCTGT 1576
CGCTTGATGA CGAGGCGGTT GCGGCCGATG TCGCCCGCAA TCTCGATCTT GCCGGGCTCG 1636
ACCGGTCGGT GCTGTCGGCC CATGCCATCG GCGAGGCGGC TTCGAAGATC GCGGTCATGC 1696
CCTCGGTGCG GCGGGCGCTG GTCGAGGCGC AGCGCAGCTT TGCGGCGCGT GAGCCGGGCA 1756
CGGTGCTGGA TGGACGCGAT ATCGGCACGG TGGTCTGCCC GGATGCGCCG GTGAAGCTCT 1816
ATGTCACCGC GTCACCGGAA GTGCGCGCGA AACGCCGCTA TGACGAAATC CTCGGCAATG 1876
GCGGGTTGGC CGATTACGGG ACGATCCTCG AGGATATCCG CCGCCGCGAC GAGCGGGACA 1936
TGGGTCGGGC GGACAGTCCT TTGAAGCCCG CCGACGATGC GCACCT 1982
```

FIG. 3E

GTAGCCACAC	ATAATTACTA	TAGTAGGAA	GCCCGCTATC	TCTCAATCCC	GCGTGATCGC	60
GCCAAAATGT	GACTGTGAAA	AATCC	ATG TCC	CAT TCT	GCA TCC CCG AAA CCA	112
	Met Ser	His Ser	Ala Ser	Pro Lys	Pro	
	1		5			
GCA ACC GCC	CGC TCG	GAG GCA	CTC ACG	GGC GAA	ATC CGC ATT CCG	160
Ala Thr	Ala Arg	Ser Glu	Ala Leu	Thr Gly	Glu Ile Arg Ile Pro	
10	15		20		25	
GGC GAC AAG	TCC ATC	TCG CAT	CGC TCC	TTC ATG	TTT GGC GGT CTC GCA	208
Gly Asp	Lys Ser	Ile Ser	His Arg	Ser Phe	Met Phe Gly Gly Leu Ala	
	30		35		40	
TCG GGC GAA	ACC CGC	ATC ACC	GGC CTT	CTG GAA	GGC GAG GAC GTC ATC	256
Ser Gly	Glu Thr	Arg Ile	Thr Arg	Leu Leu	Glu Gly Glu Asp Val Ile	
45		50		55		
AAT ACA GGC	CGC GCC	ATG CAG	GCC ATG	GGC GCG	AAA ATC CGT AAA GAG	304
Asn Thr	Gly Arg	Ala Met	Gln Ala	Met Gly	Ala Lys Ile Arg Lys Glu	
60	65		70			
GGC GAT GTC	TGG ATC	AAC AAC	GGC GTC	GGC AAT	GGC TGC CTG TTG CAG	352
Gly Asp	Val Trp	Ile Ile	Asn Asn	Gly Val	Gly Cys Leu Leu Gln	
75	80		85			

FIG. 4A

CCC GAA GCT GCG CTC GAT TTC GGC AAT GCC GGA ACC GGC GCG CTC	400
Pro Glu Ala Ala Ser Leu 95	
90	
ACC ATG GGC CTT GTC GGC ACC TAT GAC ATG AAG ACC TCC TTT ATC GGC	448
Thr Met Gly Leu Val 110	
115	
GAC GCC TCG CTG TCG AAG CCG CCG ATG GGC CGC GTG CTG AAC CCG TTG	496
Asp Ala Ser Leu Ser Lys Arg Pro Met Gly Arg Val Leu 135	
130	
CGC GAA ATG GGC GTT CAG GTG GAA GCA GCC GAT GGC GAC CGC ATG CCG	544
Arg Glu Met Gly Val Gln Val 145	
140	
CTG ACG CTG ATC GGC CCG AAG ACG GCC AAT CCG ATC ACC TAT CGC GTG	592
Leu Thr Leu Ile Gly Pro Lys 160	
155	
CCG ATG GCC TCC GCG CAG GTA AAA TCC GCC GTG CTG CTC GGT CTC	640
Pro Met Ala Ser Ala Gln Val 175	
170	
AAC ACG CCG GGC GTC ACC ACC GTC ATC GAG CCG GTC ATG ACC CGC GAC	688
Asn Thr Pro Gly Val Thr 190	
195	
200	

FIG. 4B

CAC ACC GAA AAG ATG CTG CAG GGC TTT GGC GCC GAC CTC ACG GTC GAG	736
His Thr Glu Lys 205	
ACC GAC AAG GAT GGC GTG CGC CAT ATC CGC ATC ACC GGC CAG GGC AAG	784
Thr Asp Lys 220	
CTT GTC GGC CAG ACC ATC GAC GTG CCG GGC GAT CCG TCA TCG ACC GCC	832
Leu Val 235	
TTC CCG CTC GTT GCC GCC CTT CTG GTG GAA GGT TCC GAC GTC ACC ATC	880
Phe Pro Leu Val 225	
CGC AAC GTG CTG ATG AAC CCG ACC CGT ACC GGC CTC ATC CTC ACC TTG	928
Arg Asn Val Leu 270	
CAG GAA ATG GGC GCC GAT ATC GAA GTG CTC AAT GCC GGC CTT GCA GGC	976
Gln Glu Met 285	
GGC GAA GAC GTC GCC GAT CTG CGC GTC AGG GCT TCG AAG CTC AAG GGC	1024
Gly Glu Asp Val 300	

FIG. 4C

FIG. 4D

ATC GCC ACG TCC TTC CCC GAA TTC ATG GAC ATG ATG CCG GGA TTG GGC Ile Ala Thr Ser Phe Pro Glu Phe Met Asp Met Met Pro Gly Leu Gly 430 435 440	1408
GCA AAG ATC GAG TTG AGC ATA CTC TAGTCACTCG ACAGCGAAAA TATTATTTC Ala Lys Ile Glu Leu Ser Ile Leu 445	1462
GAGATTGGGC ATTATTACCG GTTGGTCTCA GCGGGGGTTT AATGTCCAAT CTTCATACG TAACAGCATC AGGAAATATC AAAAAAGCTT TAGAAGGAAT TGCTAGAGCA GCGACGCCGC CTAAGCTTTC TCAAGACTTC GTTAAAACTG TACTGAAATC CCGGGGGGTC CGGGGATCAA ATGACTTCAT TTCTGAGAAA TTGGCCTCGC A	1522 1582 1642 1673

FIG. 4E

GTGATCGCGC CAAATGTGA CTGTGAAAAA TCC ATG TCC CAT TCT GCA TCC CCG	54
Met Ser His Ser Ala Ser Pro	5
AAA CCA GCA ACC GCC CGC TCG GAG GCA CTC ACG GGC GAA ATC CGC	102
Lys Pro Ala Thr Ala Arg Arg Ser Glu Ala Leu Thr Gly Glu Ile Arg	20
ATT CCG GGC GAC AAG TCC ATC TCG CAT CGC TCC TTC ATG TTT GGC GGT	150
Ile Pro Gly Asp Lys Ser Ile Ser His Arg Ser Phe Met Phe Gly Gly	35
CTC GCA TCG GGC GAA ACC CGC ATC ACC GGC CTT CTG GAA GGC GAG GAC	198
Leu Ala Ser Gly Glu Thr Arg Ile Thr Gly Leu Leu Glu Gly Glu Asp	55
GTC ATC AAT ACA GGC CGC GCC ATG CAG GCC ATG GGC GCG AAA ATC CGT	246
Val Ile Asn Thr Gly Arg Ala Met Gln Ala Met Gly Ala Lys Ile Arg	70
AAA GAG GGC GAT GTC TGG ATC ATC AAC GGC GTC GGC AAT GGC TGC CTG	294
Lys Glu Gly Asp Val Trp Ile Ile Asn Gly Val Gly Asn Gly Cys Leu	85
TTG CAG CCC GAA GCT GCG CTC GAT TTC GGC AAT GCC GGA ACC GGC GCG	342
Leu Gln Pro Glu Ala Ala Leu Asp Phe Gly Asn Ala Gly Thr Gly Ala	100

FIG. 5A

CGC CTC ACC ATG GGC CTT GTC GGC ACC TAT GAC ATG AAG ACC TCC TTT	390
Arg Leu 105 Thr Met Gly Leu 110 Val Gly Thr Asp Met 115 Lys Thr Ser Phe	
ATC GGC GAC GCC TCG CTG TCG AAG CGC CGC ATG GGC CGC GTG CTG AAC	438
Ile Gly 120 Asp Ala Ser Leu 125 Ser Leu 130 Met Gly Arg Val Leu Asn 135	
CCG TTG CGC GAA ATG GGC GTT CAG GTG GAA GCA GCC GAT GGC GAC CGC	486
Pro Leu Arg Glu Met 140 Val Gln Val Glu Ala Ala Asp Gly Asp Arg 150	
ATG CCG CTG ACG CTG ATC GGC CCG AAG ACG GCC AAT CCG ATC ACC TAT	534
Met Pro Leu 155 Thr Leu Ile Gly Pro 160 Lys Thr Ala Asn Pro Ile Thr Tyr 165	
CGC GTG CCG ATG GCC TCC GCG CAG GTA AAA TCC GCC GTG CTG CTC GCC	582
Arg Val 170 Pro Met Ala Ser Ala Gln 175 Val Lys Ser Ala Val Leu Ala 180	
GGT CTC AAC ACG CCG GGC GTC ACC ACC GTC ATC GAG CCG GTC ATG ACC	630
Gly Leu 185 Asn Thr Pro Gly Val 190 Thr Thr Val Ile Glu 195 Pro Val Met Thr 195	
CGC GAC CAC ACC GAA AAG ATG CTG CAG GGC TTT GGC GCC GAC CTC ACG	678
Arg Asp 200 His Thr Glu Lys Met Leu Gln Gly Phe 210 Gly Ala Asp Leu Thr 215	

FIG. 5B

GTC GAG ACC GAC AAG GAT GGC GTG CGC CAT ATC CGC ATC ACC GGC CAG Val Glu Thr Asp Lys Asp 220	726
GGC AAG CTT GTC GGC CAG ACC ATC GAC GTG CCG GGC GAT CCG TCA TCG Gly Lys Leu Val 235	774
ACC GCC TTC CCG CTC GTC GGC GAT GGC GAA GGT TCC GAC GTC Thr Ala Phe 250	822
ACC ATC CGC AAC GTG CTG ATG AAC CCG ACC CGT ACC GGC CTC ATC CTC Thr Ile Arg Asn Val 265	870
ACC TTG CAG GAA ATG GGC GGC GAT ATC GAA GTG CTC AAT GCC CGT CTT Thr Leu Glu Met 285	918
GCA GGC GGC GAA GAC GTC GGC GAT CTG CGC GTC AGG GCT TCG AAG CTC Ala Gly Gly Glu Asp 300	966
AAG GGC GTC GTC GTC GGC GAA CCG GAT GCG CCG CTG ATG ATC GAC GAA Lys Gly Val Val 315	1014

FIG. 5C

TAT CCG GTC CTG GCG ATT GCC GCC TTC TCC TCC TTC GCG GAA GGC GAA ACC GTG Tyr Pro Val 330 Leu Ala Ile Ala Ala Ser Phe Ala Glu Gly Thr Val	1062
ATG GAC GGG CTC GAC GAA GAA CTG CGC GTC AAG GAA TCG GAT CGT CTG GCA Met Asp 345 Gly Leu Asp Glu Leu Arg Val Lys Glu Ser Asp Arg Leu Ala	1110
GCG GTC GCA CGC GGC CTT GAA GCC AAC GGC GTC GAT TGC ACC GAA GGC Ala Val Ala Arg Gly Leu 365 Glu Ala Asn Gly Val Asp Cys Thr Glu Gly 375	1158
GAG ATG TCG CTG ACG GTT CGC GGC CGC CCC GGC AAG GGA CTG GGC Glu Met Ser Leu Thr Val 380 Thr Val Arg Gly Arg Pro Asp Gly Lys Gly Leu Gly 390	1206
GGC GGC ACG GTT GCA ACC CAT CTC GAT CAT CAT CGT ATC GCG ATG AGC TTC Gly Gly Thr Val 395 Val Ala Thr His Asp 400 His Arg Ile Ala Met Ser Phe 405	1254
CTC GTG ATG GGC CTT GCG GCG GAA AAG CCG GTG ACG GTT GAC GAC AGT Leu Val Met Gly Leu Ala Ala Glu 415 Lys Pro Val Thr Val Asp Asp Ser 420	1302
AAC ATG ATC GCC ACG TCC TTC CCC GAA TTC ATG GAC ATG ATG CCG GGA Asn Met Ile Ala Thr Ser 430 Phe Pro Glu Phe Met Met Met Pro Gly 435	1350

FIG. 5D

TTG GGC GCA AAG ATC GAG TTG AGC ATA CTC TAGTCACTCG ACAGCGAAAA	1400
Leu Gly Ala Lys Ile Glu Leu Ser Ile Leu	
440	
445	
TATTATTTCG GAGATTGGGC ATTATTACCG GTTGGTCTCA GCGGGGGTTT AATGTCCAAT	1460
CTTCCATACG TAACAGCATC AGGAAATATC AAAAAAGCTT	1500

FIG. 5E

1 MSHGASSRPATARKSSGLSGTVRIPGDKSISHRSFMFGGLASGETRITGL 50
1MESLTLPQIARVDGTINLPGSKTVSNRALLAALAHGKTVLTNL 44
51 LEGEDVINTGKAMQAMGARIRKEGDTWIIDGVGNNGGLLAPEAPLD..FGN 98
45 LDSDDVRHMLNALTALGVSYTL SADRTRCEIIGNGGPLHAEGALELFLGN 94
99 AATGCRLTMGLVGVDYDFDSTFIGDASLTKRPMGRVLNPLREMGVQVK.SÉ 147
95 AGTAMRPLAAALCLGSNDIVLTGEPRMKERPIGHLVDA LRLGGAKITYLE 144
148 DGDRLPVTLRGPKTPTPTITYRVPMA SAQKSAVLLAGLNTPGITTVEPI 197
145 QENYPPLRLQGGFTGGNVDDV DGSVSSQFLTALLMTAPLAPEDTVIRIKGD 194
198 MTRDHTKMLQGFGANLTVÉTDADGVRTIRLEGRGKLTGQVIDVPGDPSS 247
195 LVSKPYIDITLNL MKTFGVEIENQH YQQFVVKGGQSYQSPGTYLVEGDAS 244

FIG. 6A

248 TAFPLVAALLVPGSDVTILNVLMNPTRTGLILT..LQEMGADIEVINPRL 295
245 SASYFLAAAAIKGGTVKVTGIGRNSMQGDIRFADVLEKMGATI..... 287
296 AGGEDVADLRVRSSTLKGVTPEDRAPSMIDEYPILAVAAFAEGATVMN 345
288 CWGDDY..ISCTRGELNAIDMDMINHIP...DAAMTIATAALFAKGTTRLR 332
346 GLEELRVKESDRLSAVANGKLNGVDCDEGETSLVWRGPDGKGLGNASG 395
333 NIYNWRVKETDRLFAMATELRKVGAEEVEEGHDYIRI.TPPEKLN..... 376
396 AAVATHLDHRIAMSFVLMGLVSENPTVDDATMIATSFPEFMDLMAGLGA 445
377 AEIATYNDHRMAMCFSLVAL.SDTPVTILDPKCTAKTFPDYFEQLARISQ 425
446 KIELSDTKAA* 456
426 AA* 428

FIG. 6B

FIG. 7A

FIG. 7B

```
CCATGGCTCA CCGTGCAAGC AGCCGTCCAG CAACTGCTCG TAAGTCCTCT GGTCTTTCTG 60
GAACCGTCCG TATTCAGGT GACAAGTCTA TCTCCACAG GTCCTTCATG TTTGGAGGTC 120
TCGCTAGCGG TGAAACTCGT ATCACCGGTC TTTTGAAGG TGAAGATGTT ATCAACACTG 180
GTAAGGCTAT GCAAGCTATG GGTGCCAGAA TCCGTAAGGA AGGTGATACT TGGATCATTG 240
ATGGTGTGG TAACGGTGA CTCCTTGC TCAGGGCTCC TCICGATTTC GGTAAACGCTG 300
CAACTGGTTG CCGTTTGACT ATGGGICTTG TTGGTGTTTA CGATTTTCGAT AGCACTTTCA 360
TTGGTGACGC TTCTCTCACT AAGCGTCCAA TGGGTCGTGT GTTGAACCCA CTTGCGGAAA 420
TGGGTGTGCA GGTGAAGTCT GAAGACGGTG ATCGTCTTCC AGTTACCTTG CGTGGACCAA 480
AGACTCCAAC GCCAATCACC TACAGGGTAC CTATGGCTTC CGCTCAAGTG AAGTCCGCTG 540
TTCGTCTTGC TGGTCTCAAC ACCCCAGGTA TCACCACTGT TATCGAGCCA ATCATGACTC 600
GTGACCACAC TGAAAAGATG CTTCAAGTT TTGGTGCTAA CCTTACCGTT GAGACTGATG 660
CTGACGGTGT GCGTACCATC CGTCTTGAAG GTCGTGGTAA GCTCACCGGT CAAGTGATTG 720
ATGTTCCAGG TGATCCCTCC TCTACTGCTT TCCCATTTGGT TGCTGCCTTG CTTGTTCCAG 780
GTTCCGACGT CACCATCCTT AACGTTTTGA TGAACCCAAC CCGTACTGGT CTCATCTTGA 840
```

FIG. 8A

CTCTGCAGGA AATGGGTGCC GACATCGAAG TGATCAACCC ACGTCTTGCT GGTGGAGAAG 900
ACGTGGCTGA CTTGCGTGTT CGTTCCTTCTA CTTTGAAGGG TGTTACTGTT CCAGAAGACC 960
GTGCTCCCTC TATGATCGAC GAGTATCCAA TTCTCGCTGT TGCAGCTGCA TTCGCTGAAG 1020
GTGCTACCGT TATGAACGGT TTGGAAGAAC TCCGIGTTAA GGAAAGCGAC CGTCTTTCTG 1080
CTGTGCGCAA CGGTCTCAAG CTC AACGGTG TTGATTGCCA TGAAGGTGAG ACTTCTCTCG 1140
TCGTGCGTGG TCGTCCTGAC GGTAAGGGTC TCGGTAAACGC TTCTGGAGCA GCTGTCGCTA 1200
CCCACCTCGA TCACCGTATC GCTATGAGCT TCCTCGTTAT GGGTCTCGTT TCTGAAAACC 1260
CTGTTACTGT TGATGATGCT ACTATGATCG CTA TAGCTT CCCAGAGTTC ATGGATTGTA 1320
TGGCTGGTCT TGGAGCTAAG ATCGAACTCT CCGACACTAA GGCTGCTTGA TGAGCTC 1377

FIG. 8B

CTCTGCAGGA AATGGGTGCC GACATCGAAG TGATCAACCC ACGTCTTGCT GGTGGAGAAG 900
ACGTGGCTGA CTTGCGTGTT CGTTCTTCTA CTTTGAAGGG TGTTACTGTT CCAGAAGACC 960
GTGCTCCTTC TATGATCGAC GAGTATCCAA TTCTCGCTGT TGCAGCTGCA TTCGCTGAAG 1020
GTGCTACCGT TATGAACGGT TTGGAAGAAC TCCGTGTTAA GGAAAGCGAC CGTCTTTCTG 1080
CTGTGCAAA CGGTCTCAAG CTCACGGTG TTGATTGCGA TGAAGGTGAG ACTTCTCTCG 1140
TCGTGCGTGG TCGTCCTGAC GGTAAAGGTC TCGGTAACGC TTCITGGAGCA GCTGTCGCTA 1200
CCCACCTCGA TCACCGTATC GCTATGAGCT TCCTCGTTAT GGGTCTCGTT TCTGAAAACC 1260
CTGTTACTGT TGATGATGCT ACTATGATCG CTA TAGCTT CCCAGAGTTC ATGGATTGA 1320
TGGCTGGTCT TGGAGCTAAG ATCGAACTCT CCGACACTAA GGCTGCTTGA TGAGCTC 1377

FIG. 9

AGATCTATCG	ATAAGCTTGA	TGTAATTGGA	GGAAGATCCA	AATTTTCAAT	CCCCATTCTT	60
CGATTGCTTC	AATTGAAGTT	TCTCCG	ATG GCG CAA	GTT AGC AGA	ATC TGC AAT	113
	Met	Ala	Gln	Val	Ser Arg Ile Cys Asn	
	1				5	
GGT GTG CAG AAC CCA	TCT CTT ATC	TCC AAT	CTC TCG AAA	TCC AGT CAA		161
Gly Val Gln Asn Pro	Ser Leu Ile	Ser Asn	Leu Ser	Lys Ser Ser	Gln	
10	15		20		25	
CGC AAA TCT CCC TTA	TCG GTT TCT	CTG AAG	ACG CAG	CAT CCA	CGA	209
Arg Lys Ser Pro	Leu Ser Val	Lys Leu	Gln Thr	Gln His	Pro Arg	
	30		35		40	
GCT TAT CCG ATT	TCG TCG TCG	TGG GGA	TTG AAG	AAG AGT	GGG ATG	257
Ala Tyr Pro	Ile Ser Ser	Trp Gly	Leu Lys	Lys Ser	Gly Met Thr	
	45		50		55	

FIG. 10A

TTA ATT GGC TCT GAG CTT CGT CCT CTT AAG GTC ATG TCT TCT GTT TCC	305
Leu Ile Gly Ser Glu Leu Arg Pro Ile Val Met Ser Ser Val Ser	
	70
ACG GCG GAG AAA GCG TCG GAG ATT GTA CTT CAA CCC ATT AGA GAA ATC	353
Thr Ala Glu Lys Ala Ser Glu Ile Val Leu Gln Pro Ile Arg Glu Ile	
	80
	85
TCC GGT CTT ATT AAG TTG CCT GGC TCC AAG TCT CTA TCA AAT AGA ATT	401
Ser Gly Leu Ile Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile	
	90
	95
	100
	105
C	402

FIG. 10B

FIG. 11

AGATCTGCTA	GAAATAATTT	TGTTTAACTT	TAAGAAGGAG	ATATATCC	ATG GCA CAA	57
					Met Ala Gln	
					1	
ATT AAC AAC	ATG GCT CAA	GGG ATA CAA	ACC CTT AAT	CCC AAT TCC	AAT	105
Ile Asn Asn	Met Ala Gln	Ile Gln Thr	Leu Asn	Pro Asn Ser	Asn	
5	10	15				
TTC CAT AAA	CCC CAA GTT	CCT AAA TCT	TCA AGT TTT	CTT GTT TTT	GGA	153
Phe His Lys	Pro Gln Val	Pro Lys Ser	Ser Ser Phe	Leu Val Phe	Gly	
20	25	30			35	
TCT AAA AAA	CTG AAA AAT	TCA GCA AAT	TCT ATG TTG	GTT TTT	AAA AAA	201
Ser Lys Lys	Leu Lys Asn	Ala Asn Ser	Met Leu Val	Leu Lys	Lys	
	40	45			50	

FIG. 12A

GAT TCA ATT TTT ATG CAA AAG TTT TGT TCC TTT AGG ATT TCA GCA TCA	249
Asp Ser Ile Phe 55 Met Cys Ser Phe Arg Ile Ser Ala Ser	65
GTG GCT ACA GCA CAG AAG CCT TCT GAG ATA GTG TTG CAA CCC ATT AAA	297
Val Ala Thr 70 Ala Gln Lys Pro Ser 75 Glu Ile Val Leu 80 Gln Pro Ile Lys	
GAG ATT TCA GGC ACT GTT AAA TTG CCT GGC TCT AAA TCA TTA TCT AAT	345
Glu Ile 85 Ser Gly Thr Val Lys 90 Pro Gly Ser Lys 95 Ser Leu Ser Asn	
AGA ATT C	352
Arg Ile	
100	

FIG. 12B

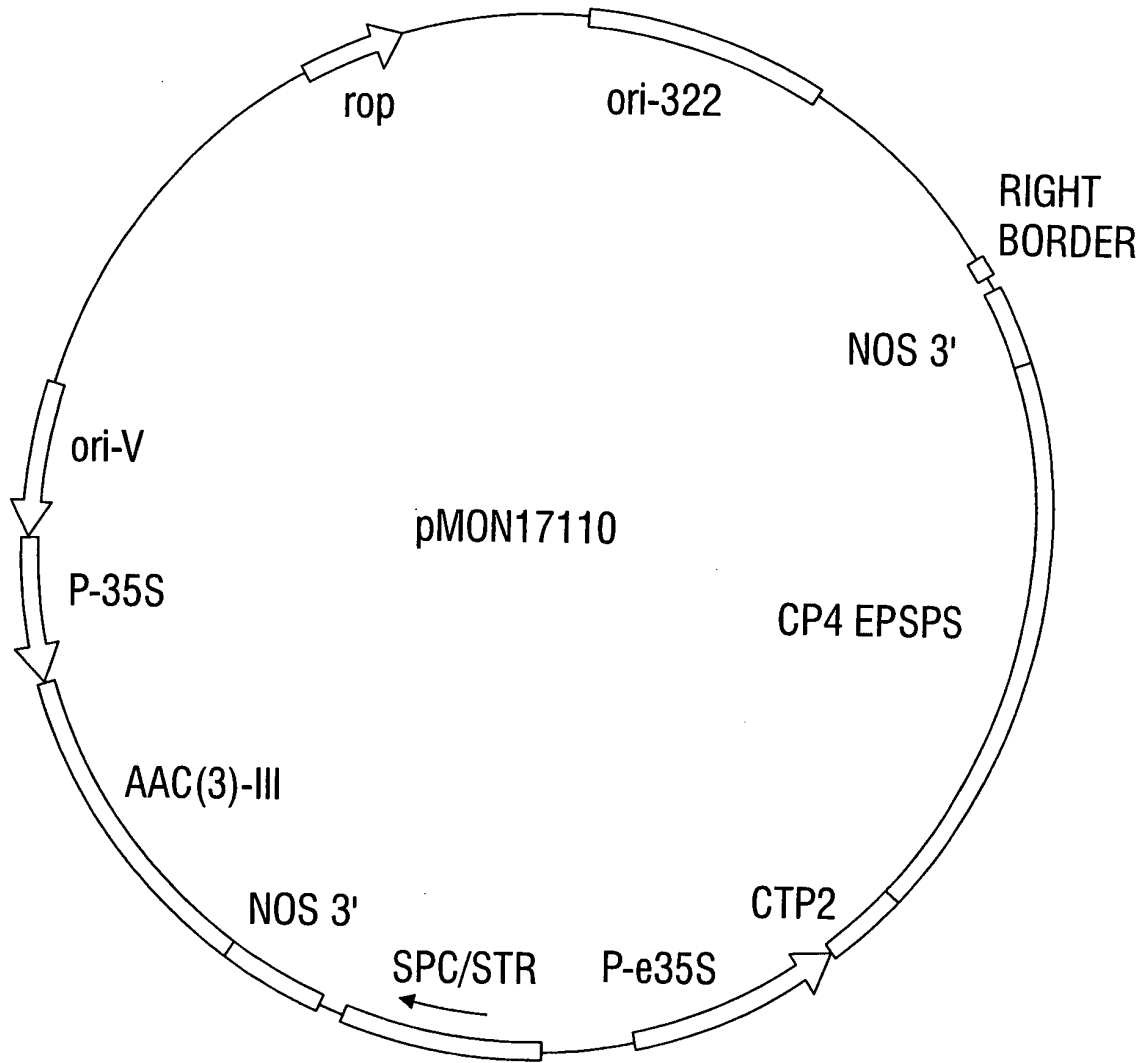


FIG. 13

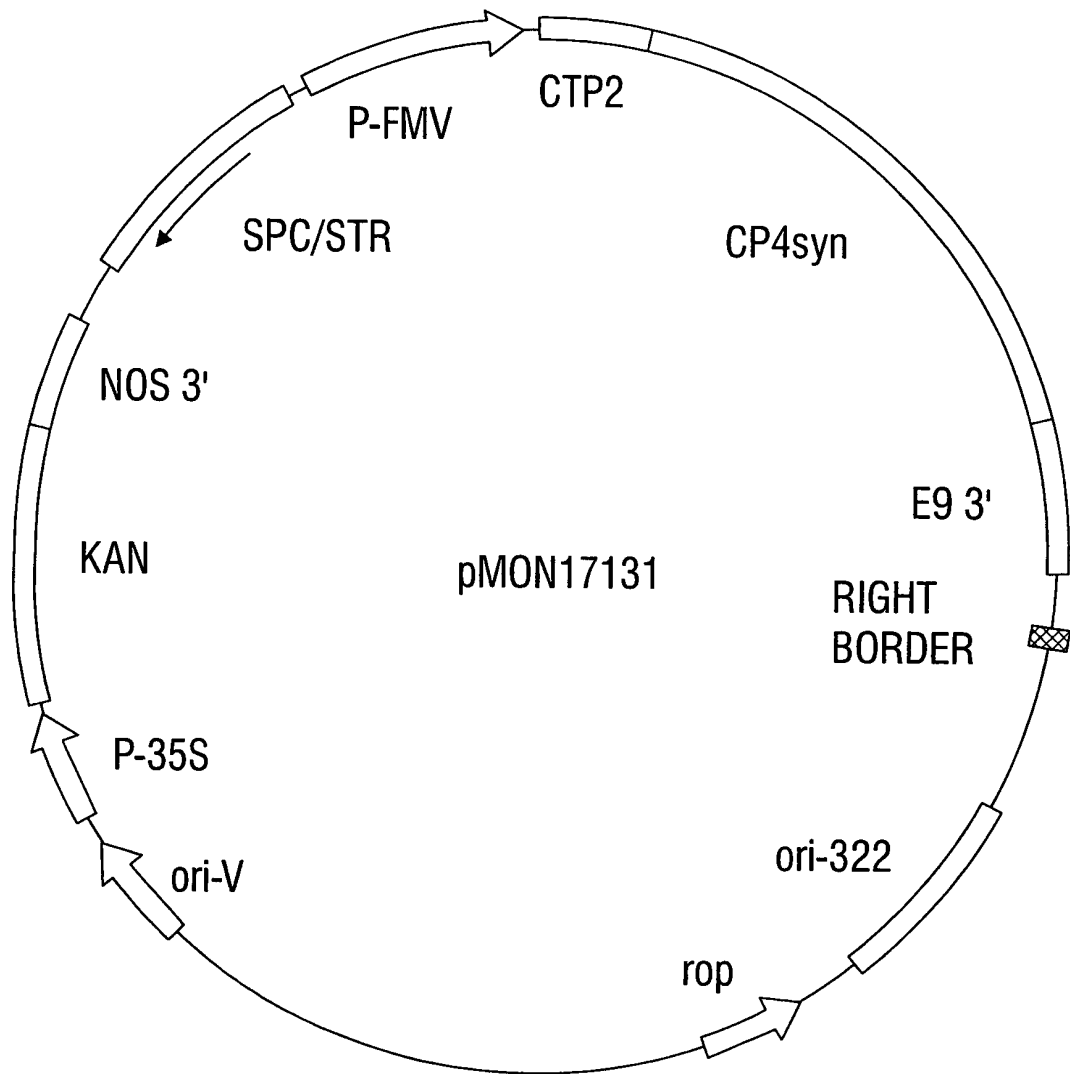


FIG. 14

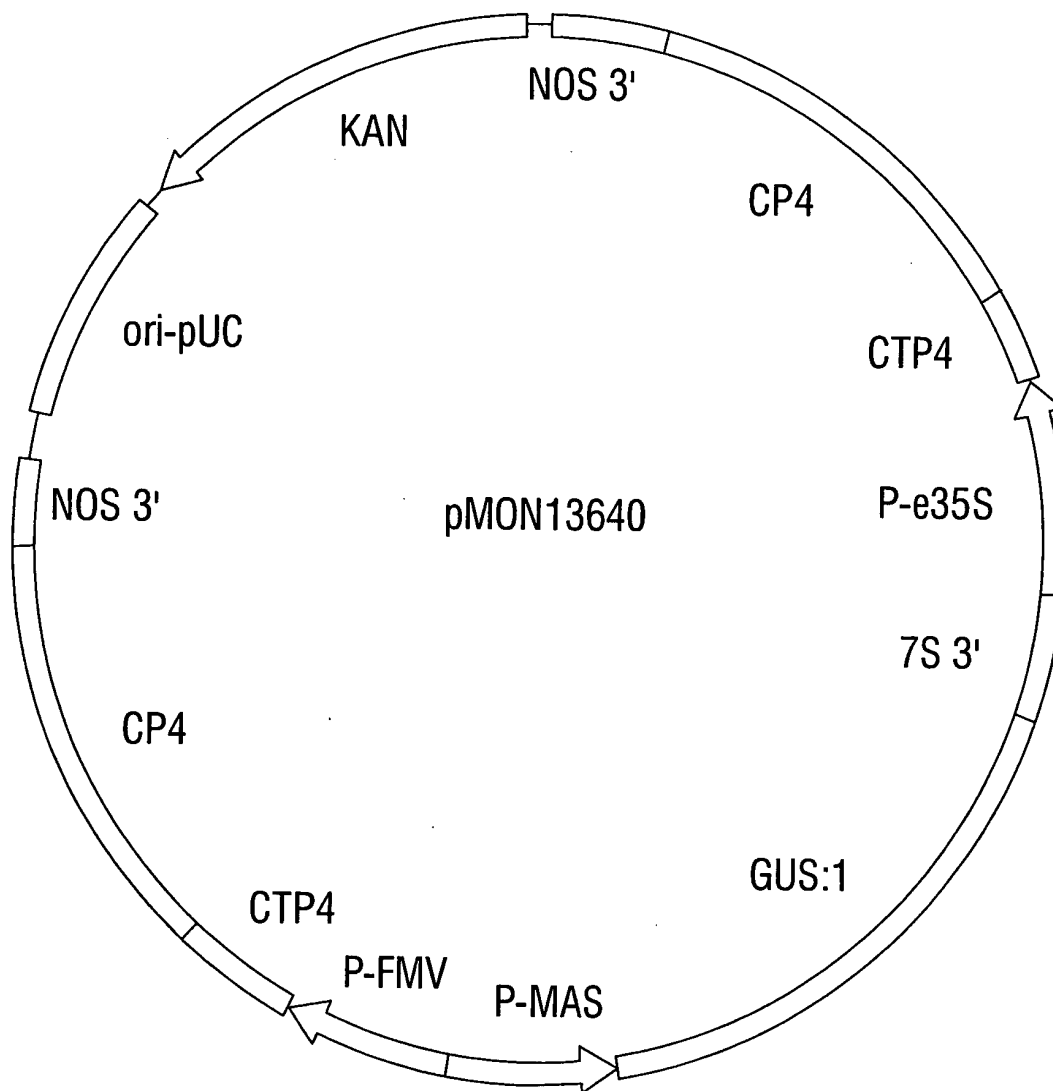


FIG. 15

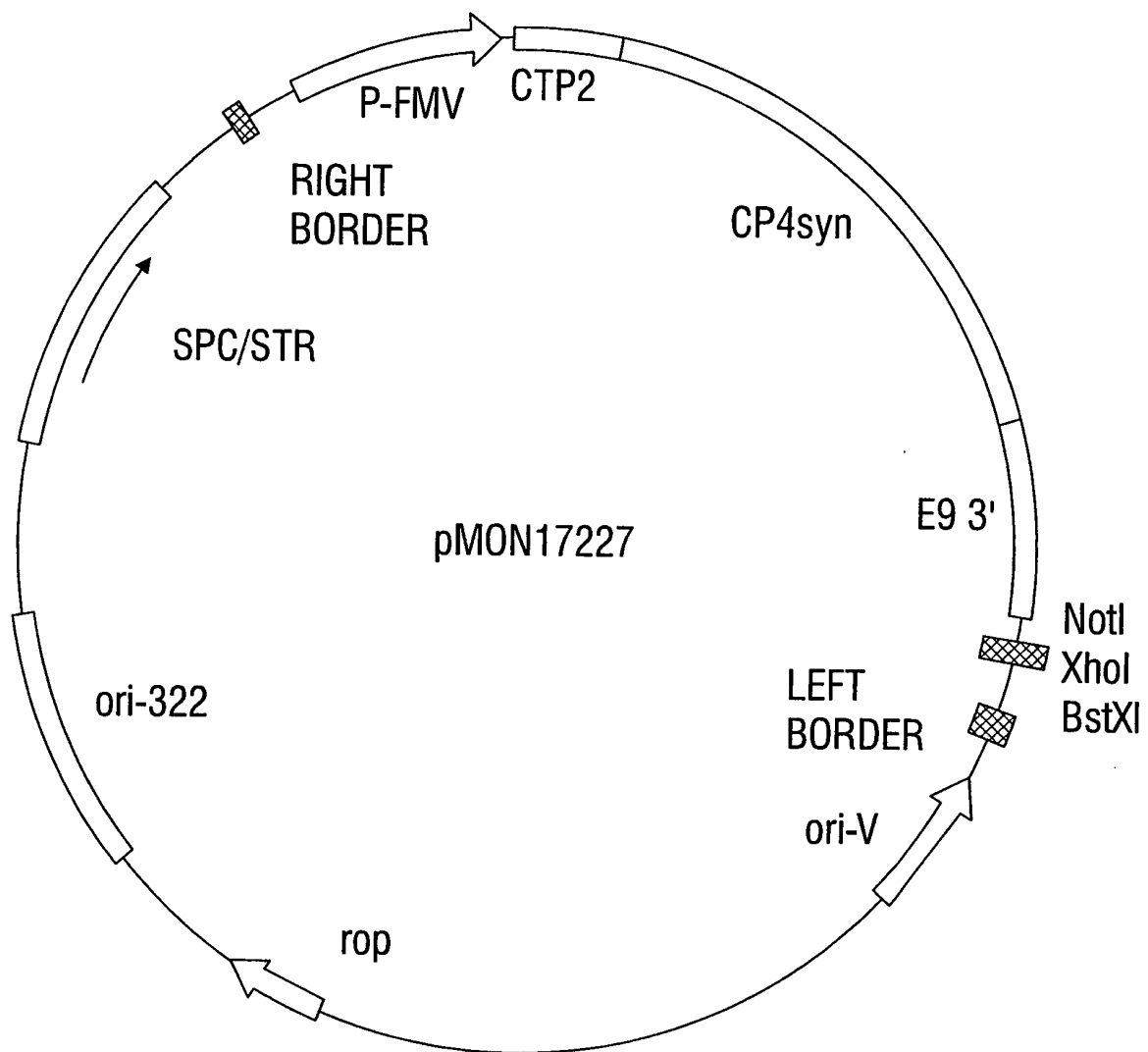


FIG. 16

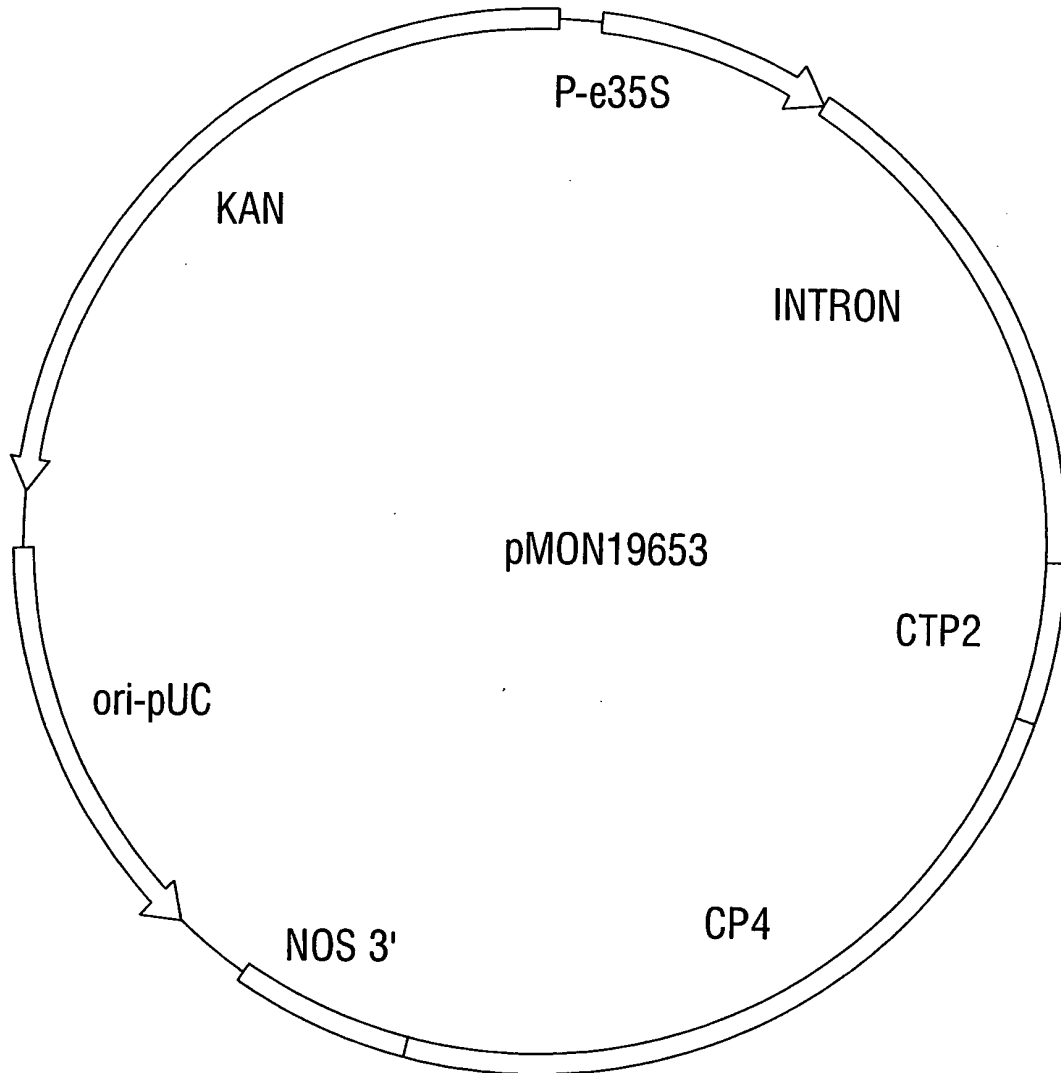


FIG. 17

ATG AAA CGA GAT AAG GTG CAG ACC TTA CAT GGA GAA ATA CAT ATT CCC Met Lys Arg Asp Lys Val Gln Thr Leu His Gly Glu Ile His Ile Pro	1 5 10 15 48
GGT GAT AAA TCC ATT TCT CAC CGC TCT GTT ATG TTT GGC GCG CTA GCG Gly Asp Lys Ser Ile Ser His Arg Ser Val Met Phe Gly Ala Leu Ala	20 25 30 96
GCA GGC ACA ACA GTT AAA AAC TTT CTG CCG GGA GCA GAT TGT CTG Ala Gly Thr Thr Val Val Lys Asn Phe Leu Pro Gly Ala Asp Cys Leu	35 40 144
AGC ACG ATC GAT TGC TTT AGA AAA ATG GGT GTT CAC ATT GAG CAA AGC Ser Thr Ile Asp Cys Phe Arg Arg Lys Met Gly Val His Ile Glu Gln Ser	50 55 60 192
AGC AGC GAT GTC GTG ATT CAC GGA AAA GGA ATC GAT GCC CTG AAA GAG Ser Ser Asp Val Val Ile Ile his Gly Lys Gly Ile Asp Ala Leu Lys Glu	65 70 75 80 240
CCA GAA AGC CTT TTA GAT GTC GGA AAT TCA GGT ACA ACG ATT CGC CTG Pro Glu Ser Ser Leu Leu Asp Val Gly Asn Ser Ser Gly Thr Thr Ile Arg Leu	85 90 95 288
ATG CTC GGA ATA TTG GCG GGC CGT CCT TTT TAC AGC GCG GTA GCC GGA Met Leu Gly Ile Leu Ala Gly Arg Pro Phe Tyr Ser Ala Val Ala Gly	100 105 110 336

FIG. 18A

GAT GAG AGC ATT GCG AAA CGC CCA ATG AAG CGT GTG ACT GAG CCT TTG	384
Asp Glu Ser Ile Ala Lys Arg Pro Met Lys Arg Val Thr Glu Pro Leu	
115 120	
AAA ATG GGG GCT AAA ATC GAC GGC AGA GCC GGA GAG TTT ACA	432
Lys Lys Met Gly Ala Lys Ile Asp Gly Arg Ala Gly Gly Glu Phe Thr	
130 135 140	
CCG CTG TCA GTG AGC GGC GCT TCA TTA AAA GGA ATT GAT TAT GTA TCA	480
Pro Leu Ser Ser Val Ser Gly Ala Ser Leu Lys Gly Ile Asp Tyr Val Ser	
145 150 155 160	
CCT GTT GCA AGC GCG CAA ATT AAA TCT GCT GTT TTG CTG GCC GGA TTA	528
Pro Val Ala Ser Ala Ser Gln Ile Lys Ser Ala Val Leu Leu Ala Gly Leu	
165 170 175	
CAG GCT GAG GGC ACA ACT ACA GAG CCC CAT AAA TCT CGG GAC	576
Gln Ala Glu Gly Thr Thr Thr Val Thr Glu Pro His Lys Ser Arg Asp	
180 185 190	
CAC ACT GAG CGG ATG CTT TCT GCT TTT GGC GTT AAG CTT TCT GAA GAT	624
His Thr Glu Arg Met Leu Ser Ala Phe Gly Val Lys Leu Ser Glu Asp	
195 200 205	
CAA ACG AGT GTT TCC ATT GCT GGT GGC CAG AAA CTG ACA GCT GCT GAT	672
Gln Thr Ser Val Ser Ile Ala Gly Gly Gln Lys Leu Thr Ala Ala Asp	
210 215 220	

FIG. 18B

ATT TTT GTT CCT GGA GAC ATT TCT TCA GCC GCG TTT TTC CTT GCT GCT	720
Ile Phe Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Phe Leu Ala Ala	240
225	
GGC GCG ATG GTT CCA AAC AGC AGA ATT GTA TTG AAA AAC GTA GGT TTA	768
Gly Ala Met Val Pro Asn Ser Arg Ile Val Val Leu Lys Asn Val Gly Leu	255
245	
AAT CCG ACT CGG ACA GGT ATT ATT GAT GTC CTT CAA AAC ATG GGG GCA	816
Asn Pro Thr Arg Thr Gly Ile Ile Asp Val Val Leu Gln Asn Met Gly Ala	270
260	
AAA CTT GAA ATC AAA CCA TCT GCT GAT AGC GGT GCA GAG CCT TAT GGA	864
Lys Leu Glu Ile Lys Pro Ser Ala Asp Ser Ser Gly Ala Glu Pro Tyr Gly	285
275	
GAT TTG ATT ATA GAA ACG TCA TCT CTA AAG GCA GTT GAA ATC GGA GGA	912
Asp Leu Ile Ile Glu Thr Ser Ser Leu Lys Ala Val Glu Ile Gly Gly	300
290	
GAT ATC ATT CCG CGT TTA ATT GAT GAG ATC CCT ATC ATC GCG CTT CTT	960
Asp Ile Ile Pro Arg Leu Ile Asp Glu Ile Pro Ile Ile Ala Leu Leu	315
305	
GCG ACT CAG GCG GAA ACC ACC GTT ATT AAG GAC GCG GCA GAG CTA	1008
Ala Thr Gln Ala Glu Gly Thr Thr Val Ile Lys Asp Ala Ala Glu Leu	330
325	
335	

FIG. 18C

AAA GTG AAA GAA ACA AAC CGT ATT GAT ACT GTT GTT TCT GAG CTT CGC	1056
Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Val Val Ser Glu Leu Arg	
340 345 350	
AAG CTG GGT GCT GAA ATT GAA CCG ACA GCA GAT GGA ATG AAG GTT TAT	1104
Lys Leu Gly Ala Glu Ile Glu Pro Thr Ala Asp Gly Met Lys Val Tyr	
355 360 365	
GGC AAA CAA ACG TTG AAA GGC GGC GCT GCA GTG TCC AGC CAC GGA GAT	1152
Gly Lys Gln Thr Thr Leu Lys Gly Gly Ala Ala Val Ser Ser His Gly Asp	
370 375 380	
CAT CGA ATC GGA ATG ATG CTT GGT ATT GCT TCC TGT ATA ACG GAG GAG	1200
His Arg Ile Gly Met Met Leu Gly Ile Ala Ser Cys Ile Thr Glu Glu	
385 390 395 400	
CCG ATT GAA ATC GAG CAC ACG GAT GCC ATT CAC GTT TCT TAT CCA ACC	1248
Pro Ile Glu Ile Glu His Thr Asp Ala Ile His Val Ser Tyr Pro Thr	
405 410 415	
TTC TTC GAG CAT TTA AAT AAG CTT TCG AAA AAA TCC TGA	1287
Phe Phe Glu His Leu Asn Lys Leu Ser Lys Lys Ser	
420 425	

FIG. 18D

ATG GTA AAT GAA CAA ATC ATT GAT ATT TCA GGT CCG TTA AAG GGC GAA Met Val Asn Glu Gln Ile Ile Asp Ile Ser Gly Pro Leu Lys Gly Glu	1 5 10 15 48
ATA GAA GTG CCG GGC GAT AAG TCA ATG ACA CAC CGT GCA ATC ATG TTG Ile Glu Val Pro Gly Asp Lys Ser Met Thr His Arg Ala Ile Met Leu	20 25 30 96
GCG TCG CTA GCT GAA GGT GTA TCT ACT ATA TAT AAG CCA CTA CTT GGC Ala Ser Leu Ala Glu Gly Val Ser Thr Ile Tyr Lys Pro Leu Leu Gly	35 40 45 144
GAA GAT TGT CGT CGT ACG ATG GAC ATT TTC CGA CAC TTA GGT GTA GAA Glu Asp Cys Arg Arg Thr Met Asp Ile Phe Arg His Leu Gly Val Glu	50 55 60 192
ATC AAA GAA GAT GAT GAA AAA TTA GTT GTG ACT TCC CCA GGA TAT CAA Ile Lys Glu Asp Asp Glu Lys Leu Val Thr Ser Pro Gly Tyr Gln	65 70 75 80 240
GTT AAC ACG CCA CAT CAA GTA TTG TAT ACA GGT AAT TCT GGT ACG ACA Val Asn Thr Pro His Gln Val Leu Tyr Thr Gly Asn Ser Gly Thr Thr	85 90 95 288
ACA CGA TTA TTG GCA GGT TTG TTA AGT GGT TTA GGT AAT GAA AGT GTT Thr Arg Leu Leu Ala Gly Leu Ser Gly Leu Gly Asn Glu Ser Val	100 105 110 336

FIG. 19A

TTG TCT GGC GAT GTT TCA ATT GGT AAA AGG CCA ATG GAT CGT GTC TTG Leu Ser Gly Asp Val Ser Ile Gly Lys Arg Pro Met Asp Arg Val Leu	384
AGA CCA TTG AAA CTT ATG GAT GCG AAT ATT GAA GGT ATT GAA GAT AAT Arg Pro Leu Lys Leu Met Asp Ala Asn Ile Glu Gly Ile Glu Asp Asn	432
TAT ACA CCA TTA ATT ATT AAG CCA TCT GTC ATA AAA GGT ATA AAT TAT Tyr Thr Pro Leu Ile Ile Lys Pro Ser Val Ile Lys Gly Ile Asn Tyr	480
CAA ATG GAA GTT GCA AGT GCA CAA GTA AAA AGT GCC ATT TTA TTT GCA Gln Met Glu Val Ala Ser Ala Gln Val Lys Ser Ala Ile Leu Phe Ala	528
AGT TTG TTT TCT AAG GAA CCG ACC ATC ATT AAA GAA TTA GAT GTA AGT Ser Leu Phe Ser Lys Glu Pro Thr Ile Ile Ile Lys Glu Leu Asp Val Ser	576
CGA AAT CAT ACT GAG ACG ATG TTC AAA CAT TTT AAT ATT CCA ATT GAA Arg Asn His Thr Glu Thr Met Phe Lys His Phe Asn Ile Pro Ile Glu	624
GCA GAA GGG TTA TCA ATT AAT ACA ACC CCT GAA GCA ATT CGA TAC ATT Ala Glu Gly Leu Ser Ile Asn Thr Pro Glu Ala Ile Arg Tyr Ile	672

FIG. 19B

AAA CCT GCA GAT TTT CAT GTT CCT GGC GAT ATT TCA TCT GCA GCG TTC Lys Pro Ala Asp Phe His Val Pro Gly Asp Ile Ser Ser Ala Ala Phe 225 230 235 240	720
TTT ATT GTT GCA GCA CTT ATC ACA CCA GGA AGT GAT GTA ACA ATT CAT Phe Ile Val Ala Ala Leu Ile Thr Pro Gly Ser Asp Val Thr Ile His 245 250 255	768
AAT GTT GGA ATC AAT CAA ACA CGT TCA GGT ATT ATT GAT ATT GTT GAA Asn Val Gly Ile Asn Gln Thr Arg Ser Ser Gly Ile Ile Asp Ile Val Glu 260 265 270	816
AAA ATG GGC GGT AAT ATC CAA CTT TTC AAT CAA ACA ACT GGT GCT GAA Lys Met Gly Gly Asn Ile Gln Leu Phe Asn Thr Thr Gly Ala Glu 275 280 285	864
CCT ACT GCT TCT ATT CGT ATT CAA TAC ACA CCA ATG CTT CAA CCA ATA Pro Thr Ala Ser Ile Arg Ile Gln Tyr Thr Pro Met Leu Gln Pro Ile 290 295 300	912
ACA ATC GAA GGA GAA TTA GTT CCA AAA GCA ATT GAT GAA CTG CCT GTA Thr Ile Glu Gly Glu Leu Val Pro Lys Ala Ile Asp Glu Leu Pro Val 305 310 315 320	960
ATA GCA TTA CTT TGT ACA CAA GCA GTT GGC ACG AGT ACA ATT AAA GAT Ile Ala Leu Leu Cys Thr Gln Ala Val Gly Thr Ser Thr Ile Lys Asp 325 330 335	1008

FIG. 19C

GCC GAG GAA TTA AAA GTA AAA GAA ACA AAT AGA ATT GAT ACA ACG GCT Ala Glu Glu Leu Lys Val Lys Glu Thr Asn Arg Ile Asp Thr Thr Ala	1056
GAT ATG TTA AAC TTG TTA GGG TTT GAA TTA CAA CCA ACT AAT GAT GGA Asp Met Leu Asn Leu Leu Leu Phe Gly Phe Glu Leu Gln Pro Thr Asn Asp Gly	1104
TTG ATT ATT CAT CCG ATA GGA ATG ATG ATG CTT GCA GTT GCT TGT GTA CTT TTA Leu Ile Ile His Pro Ser Gly Met Met Leu Ala Val Asn Ala Thr Asp Ile Leu	1152
ACT GAT CAT CGA ATA GGA ATG ATG ATG CTT GCA GTT GCT TGT GTA CTT TCA Thr Asp His Arg Ile Gly Met Met Leu Ala Val Ala Cys Val Leu Ser	1200
AGC GAG CCT GTC AAA ATC AAA CAA TTT GAT GCT GTA AAT GTA TCA TTT Ser Glu Pro Val Lys Ile Lys Gln Phe Asp Ala Val Asn Val Ser Phe	1248
CCA GGA TTT TTA CCA AAA CTA AAG CTT TTA CAA AAT GAG GGA TAA Pro Gly Phe Leu Pro Lys Leu Lys Leu Leu Gln Asn Glu Gly	1293

FIG. 19D

1	PG2982	MSHSASPKPA	TARRSEALTG	50
	LBAA	MSHSASPKPA	TARRSEALTG	
	Agrobacterium CP4	MSHGASSRPA	TARKSSGLSG	
	B. subtilisM	KRDKVQTLHG	
	S. aureusMVNEQ	IIDISGPLKG	
	S. cerevisiaeLVYP	FKDIPADQKQ	
	A. nidulansVHP	..GVAHSSNV	
	B. napusK...	ASEI VLQPIREISG	
	A. thalianaK...	ASEI VLQPIREISG	
	N. tabacumK...	PNEI VLQPIKDISG	
	L. esculentumK...	PHEI VLXPIKDISG	
	P. hybridaK...	PSEI VLQPIKEISG	
	Z. maysAGAEI	VLQPIKEISG	
	S. gallinarumMESL	TLQPIARVDG	
	S. typhimuriumMESL	TLQPIARVDG	
	S. typhiMESL	TLQPIARVDG	
	E. coliMESL	TLQPIARVDG	
	K. pneumoniaeMESL	TLQPIARVDG	
	Y. enterocoliticaMLESL	TLHPIALING	
	H. influenzaeMEKI	TLAPISAVEG	
	P. multocidaMIKDATAI	TLNPISYIEG	
	A. salmonicidaNSL	RLEPISRVA	
	B. pertussisMSGLAYL	DLPAARLARG	
	Consensus	

FIG. 20A

51	PG2982	EIRIPGDKSI	SHRSFMFGGL	ASGETRITGL	LEGEDVINTG	RAMQAM.GAK
	LBAA	EIRIPGDKSI	SHRSFMFGGL	ASGETRITGL	LEGEDVINTG	RAMQAM.GAK
	Agrobacterium CP4	TVRIPGDKSI	SHRSFMFGGL	ASGETRITGL	LEGEDVINTG	KAMQAM.GAR
	B. subtilis	EIHIPGDKSI	SHRSVMFGAL	AAGTTTVKNF	LPGADCLSTI	DCFRKM.GVH
	S. aureus	EIEVPGDKSM	THRAIMLASL	AEGVSTIYKP	LLGEDCRRTM	DIFRHL.GVE
	S. cerevisiae	VVIPP G SKSI	SNRALILAAL	GEGQCKIKNL	LHSDDTKHML	TAVHELKGAT
	A. nidulans	ICAPPGSKSI	SNRALVLAAL	GSGETCRIKNL	LHSDDTTEVML	NALERLGAAT
	B. napus	LIKLP G SKSL	SNRI L LLAAL	SEGTTVVDNL	LNSSDDINMYL	DALKKL.GLN
	A. thaliana	LIKLP G SKSL	SNRI L LLAAL	SEGTTVVDNL	LNSSDDINMYL	DALKrL.GLN
	N. tabacum	TVKLP G SKSL	SNRI L LLAAL	SKGRTVVDNL	LSSDDIHMYL	GALKTL.GLH
	L. esculentum	TVKLP G SKSL	SNRI L LLAAL	SEGRTVVDNL	LSSDDIHMYL	GALKTL.GLH
	P. hybrida	TVKLP G SKSL	SNRI L LLAAL	SEGTTVVDNL	LSSDDIHMYL	GALKTL.GLH
	Z. mays	TVKLP G SKSL	SNRI L LLAAL	SEGTTVVDNL	LNSEDDVHYML	GALRTL.GLS
	S. gallinarum	AINLP G SKSV	SNRALLAAL	ACGKTVLTNL	LDSDDVHRHML	NALSAL.GIN
	S. typhimurium	AINLP G SKSV	SNRALLAAL	PCGKTALTNL	LDSDDVHRHML	NALSAL.GIN
	S. typhi	AINLP G SKSV	SNRALLAAL	ACGKTVLTNL	LDSDDVHRHML	NALSAL.GIN
	E. coli	TINLP G SKTV	SNRALLAAL	AHGKTVLTNL	LDSDDVHRHML	NALTAL.GVS
	K. pneumoniae	TVNLP G SKSV	SNRALLAAL	ARGTTVLTNL	LDSDDVHRHML	NALSAL.GVH
	Y. enterocolitica	TVNLP G SKSV	SNRALLAAL	AEGTTQLNNL	LDSDDIRHML	NALQAL.GVK
	H. influenzae	TINLP G SKSL	SNRALLAAL	AKGTTKVTLN	LDSDDIRHML	NALKAL.GVR
	P. multocida	EVRLP G SKSL	SNRALLSAL	AKGKTTLTNL	LDSDDVHRHML	NALKEL.GVT
	A. salmonicida	EVNLP G SKSV	SNRALLAAL	ARGTTRLTNL	LDSDDIRHML	AALTQL.GVK
	B. pertussis	EVALP G SKSI	SNRVLLAAL	AEGSTEITGL	LDSDDTRVML	AALRQL.GVS
	Consensus	----PG-K--	--R-----L	--G-----	L----D-----	-----

FIG. 20B

PG2982	IRKEGDVWII	NGVNGCCLLQ	P.....EAA	LDFGNAGTGA	RLTMGLVGTY	150
LBAA	IRKEGDVWII	NGVNGCCLLQ	P.....EAA	LDFGNAGTGA	RLTMGLVGTY	
Agrobacterium CP4	IRKEGDTWII	DGVNGGGLLA	P.....EAP	LDFGNAATGC	RLTMGLVGTV	
B. subtilis	IEQSSSDVVI	HGKGIDALKE	P.....ESL	LDVNSGTTI	RLMLGILAGR	
S. aureus	IKEDDEKLW	TSPGYQ.VNT	P.....HQP	LYTNSGTTT	RLLAGLLSGL	
S. cerevisiae	ISWEDNGETV	VVEGHGG...	.STLSACADP	LYLGNAGTAS	RFLTSLAALV	
A. nidulans	FSWEEEGEVL	VVNGKGG...	.NLQASSP	LYLGNAGTAS	RFLTTVATLA	
B. napus	VERDSVNNRA	VVEGCGGIFP	.ASLDSKSDIE	LYLGNAGTAM	RPLTAAVTAA	
A. thaliana	VETDSENNRA	VVEGCGGIFP	.ASIDSKSDIE	LYLGNAGTAM	RPLTAAVTAA	
N. tabacum	VEDDNENQRA	IVEGCGGQFP	.VGKKSEEEIQ	LFLGNAGTAM	RPLTAAVTVA	
L. esculentum	VEDDNENQRA	IVEGCGGQFP	.VGKKSEEEIQ	LFLGNAGTAM	RPLTAAVTVA	
P. hybrida	VEEDSANQRA	VVEGCGGLFP	.VGKESKEEIQ	LFLGNAGTAM	RPLTAAVTVA	
Z. mays	VEADKAAKRA	VVVGCGGKFP	.VE.DAKEEVQ	LFLGNAGTAM	RPLTAAVTAA	
S. gallinarum	YTLSADRTTC	DITNGGGPLR	AP....GALE	LFLGNAGTAM	RPLAAALCL.	
S. typhimurium	YTLSADRTTC	DITNGGGALR	AP....GALE	LFLGNAGTAM	RPLAAALCL.	
S. typhi	YTLSADRTTC	DITNGGGPLR	AS....GTLE	LFLGNAGTAM	RPLAAALCL.	
E. coli	YTLSADRTTC	EIIGNGGPLH	AE....GALE	LFLGNAGTAM	RPLAAALCL.	
K. pneumoniae	YVLSDDRTRC	EVTGTGGPLQ	AG....SALE	LFLGNAGTAM	RPLAAALCL.	
Y. enterocolitica	YRLSADRTRC	EVDGLGKLV	AE....QPLE	LFLGNAGTAM	RPLAAALCL.	
H. influenzae	YQLSDDKTIC	EIEGLGGAFN	IQ....DNLS	LFLGNAGTAM	RPLTAALCLK	
P. multocida	YQLSEDKSVC	EIEGLGRAFE	WQ....SGLA	LFLGNAGTAM	RPLTAALCLS	
A. salmonicida	YKLSADKTEC	TVHGLGRSFA	VS....APVN	LFLGNAGTAM	RPLCAALCL.	
B. pertussis	VGEVAD...GC	VTIEGVARFP	TE....QAE	LFLGNAGTAF	RPLTAALALM	
Consensus	-----	-----	-----	L--GN--T--	R-----	

FIG. 20C

PG2982	DM.....KT	SFIGDASLSK	RPMGRVLNPL	REMGVQVEAA	DGDRMPLT..	200
LBAA	DM.....KT	SFIGDASLSK	RPMGRVLNPL	REMGVQVEAA	DGDRMPLT..	
Agrobacterium CP4	DF.....DS	TFIGDASLTK	RPMGRVLNPL	REMGVQVKSE	DGDRLPVT..	
B. subtilis	PF.....YS	AVAGDESIK	RPMKRVTEPL	KMGAKIDGR	AGGEFTPL..	
S. aureus	GN.....ES	VLSGDVSIGK	RPMDRVLRPL	KLMDANIEG.	IEDNYTPL..	
S. cerevisiae	NST.SSQKYI	VLGTGNARMQ	RPIAPLVDSL	RANGTKIEYL	NNEGSLPIKV	
A. nidulans	NS..STVDSS	VLGTGNRMKQ	RPIGDLVDAL	TANVLPNTS	KGRASLPLKI	
B. napus	G....GNASY	VLDGVPRMRE	RPIGDLVVGL	KQLGADVECT	LGTCNCPVVRV	
A. thaliana	G....GNASY	VLDGVPRMRE	RPIGDLVVGL	KQLGADVECT	LGTCNCPVVRV	
N. tabacum	G....GHSRY	VLDGVPRMRE	RPIGDLVDGL	KQLGAEVDCF	LGTCNCPVRI	
L. esculentum	G....GHSRY	VLDGVPRMRE	RPIGDLVDGL	KQLGAEVDCS	LGTCNCPVRI	
P. hybrida	G....GNSRY	VLDGVPRMRE	RPIGDLVDGL	KQLGAEVDCF	LGTCNCPVRI	
Z. mays	G....GNATY	VLDGVPRMRE	RPIGDLVVGL	KQLGADVDCF	LGTCNCPVVRV	
S. gallinarumGQNEI	VLTEPRMKE	RPIGHLVDSL	RQGGANIDYL	EQENYPPLRL	
S. typhimuriumGQNEI	VLTEPRMKE	RPIGHLVDSL	RQGGANIDYL	EQENYPPLRL	
S. typhiGQNEI	VLTEPRMKE	RPIGHLVDSL	RQGGANIDYL	EQENYPPLRL	
E. coliGSNDI	VLTEPRMKE	RPIGHLVDAL	RLGGAKITYL	EQENYPPLRL	
K. pneumoniaeGSNDI	VLTEPRMKE	RPIGHLVDAL	RQGGAQIDYL	EQENYPPLRL	
Y. enterocoliticaGKNDI	VLTEPRMKE	RPIGHLVDAL	RQGGAQIDYL	EQENYRR.CI	
H. influenzae	G.NHEV..EI	ILTGEPRMKE	RPIHLVDAL	RQAGADIRYL	ENEGYPPLAI	
P. multocida	TPNREGKENI	VLTEPRMKE	RPIQHLVDAL	CQAGAEIQYL	EQEGYPPIAI	
A. salmonicidaGSGEY	MLGGEPRMEE	RPIGHLVDCL	ALKGAHIQYL	KKDGYPPLVW	
B. pertussis	G....G DY	RLSGVPRMHE	RPIGDLVDAL	RQFGAGIEYL	GQAGYPPLRI	
Consensus	-----G-----	-----L	RP-----L	-----	-----	

FIG. 20D

PG2982	LIGPK	TANPITYRVP	MASQVKS	LLAGLN	TPGVTT
LBAA	LIGPK	TANPITYRVP	MASQVKS	LLAGLN	TPGVTT
Agrobacterium CP4	LRPK	TPTITYRVP	MASQVKS	LLAGLN	TPGITT
B. subtilis	SVSGA	SLKGIDYVSP	VASQIKS	LLAGLQ	AEGTTT
S. aureus	IIKPS	VIKGINYQME	VASQVKS	LFASLF	SKEPTI
S. cerevisiae	YTDSVFKG	GRIELAA	TVSSQVSSI	LMCAPYAE	EPVTLALVG
A. nidulans	AASGGFAG	GNINLAA	KVSSQVSSL	LMCAPYAK	EPVTLRLVG
B. napus	NANGGLPG	GKVKLSG	SISSQYLTAL	LMAAP.LA	LGDVEIEII
A. thaliana	NANGGLPG	GKVKLSG	SISSQYLTAL	LMSAP.LA	LGDVEIEIV
N. tabacum	VSKGGLPG	GKVKLSG	SISSQYLTAL	LMAAP.LA	LGDVEIEII
L. esculentum	VSKGGLPG	GKVKLSG	SISSQYLTAL	LMAAP.LA	LGDVEIEII
P. hybrida	VSKGGLPG	GKVKLSG	SISSQYLTAL	LMAAP.LA	LGDVEIEII
Z. mays	NGIGGLPG	GKVKLSG	SISSQYLSAL	LMAAP.LP	LGDVEIEII
S. gallinarum	RG.GFIG	GDIKVDG	SVSSQFLTAL	LMTAP.LA	PKDTIIRVK
S. typhimurium	RG.GFTG	GDIKVDG	SVSSQFLTAL	LMTAP.LA	PKDTIIRVK
S. typhi	RG.GFIG	GDIKVDG	SVSSQFLTAL	LMTAP.LA	PEDTIIRVK
E. coli	QG.GFTG	GNVDVDG	SVSSQFLTAL	LMTAP.LA	PEDTVIRIK
K. pneumoniae	RG.GFTG	GDIKVDG	SVSSQFLTAL	LMAAP.LA	PQDTVIAIK
Y. enterocolitica	AG.GFRG	GKLTVDG	SVSSQFLTAL	LMTAP.LA	EQDTEIQIQ
H. influenzae	RNK.GIKG	GKVKIDG	SISSQFLTAL	LMSAP.LA	ENDTEIEII
P. multocida	RNT.GLKG	GRIKIDG	SVSSQFLTAL	LMAAP.MA	EADTEIEII
A. salmonicida	DAK.GLWG	GDVHVDG	SVSSQFLTAL	LMAAPAMA	PVIPRIHIK
B. pertussis	GGGSIRVD	GPVRVEG	SVSSQFLTAL	LMAAPVLARR	SGQDITIEVV
Consensus	-----	-----	--S-Q----	L-----	-----

FIG. 20E

PG2982	251	VIEPVMTRDH	TEKMLQGFGA	DLTVETDKGD	VRHIRTGQG	KLVGQ.TIDV	300
LBAA		VIEPVMTRDH	TEKMLQGFGA	DLTVETDKDG	VRHIRTGQG	KLVGQ.TIDV	
Agrobacterium CP4		VIEPIMTRDH	TEKMLQGFGA	NLTVETDADG	VRTIRLEGRG	KLIGQ.VIDV	
B. subtilis		VTEPHKSRDH	TERMLSAFGV	KLSEDQTS..	...VSIAGGQ	KLTA.A.DIFV	
S. aureus		IKELDVSRNH	TETMFKHFNI	PIEAEGLS..	..INTTPEAI	RYIKPADFHV	
S. cerevisiae		GKPISKLYVD	MTIKMMEKFG	IN.VET.STT	EPYTYIIPKG	HYINPSEYVI	
A. nidulans		GKPISQPYID	MTTAMMRSFG	ID..VQKSTT	EEHTYHIPQG	RYVNPAEYVI	
B. napus		DKLISVPYVE	MTLKLMEFVG	VS..AEHSDS	WDRFFVKGGQ	KYKSPGNAYV	
A. thaliana		DKLISVPYVE	MTLKLMEFVG	VS..VEHSDS	WDRFFVKGGQ	KYKSPGNAYV	
N. tabacum		DKLISVPYVE	MTLKLMEFVG	VS..VEHTSS	WDKFLVRGGQ	KYKSPGKAYV	
L. esculentum		DKLISVPYVE	MTLKLMEFVG	VF..VEHSSG	WDRFLVKGGQ	KYKSPGKAFV	
P. hybrida		DKLISVPYVE	MTLKLMEFVG	IS..VEHSSS	WDRFFVRRGGQ	KYKSPGKAFV	
Z. mays		DKLISIPYVE	MTLRLMERFG	VK..AEHSDS	WDRFYIKGGQ	KYKSPKNAYV	
S. gallinarum		GELVSKPYID	ITLNLTKTFG	VE..IAN.HH	YQQFVVKGGQ	QYHSPGRYLV	
S. typhimurium		GELVSKPYID	ITLNLTKTFG	VE..IAN.HH	YQQFVVKGGQ	QYHSPGRYLV	
S. typhi		GELVSKPYID	ITLNLTKTFG	VE..IAN.HH	YQQFVVKGGQ	QYHSPGRYLV	
E. coli		GDLVSKPYID	ITLNLTKTFG	VE..IEN.QH	YQQFVVKGGQ	SYQSPGTYL	
K. pneumoniae		GELVSRPYID	ITLHLMKTFG	VE..VEN.QA	YQRFIVRGNG	QYQSPGDYLV	
Y. enterocolitica		GELVSKPYID	ITLHLMKAFG	VD..VVH.EN	YQIFHIKGGQ	TYRSPGIYLV	
H. influenzae		GELVSKPYID	ITLAMMRDFG	VK..VEN.HH	YQKFQVKGNQ	SYISPNKYLV	
P. multocida		GELVSKPYID	ITLKM MQTFG	VE..VEN.QA	YQRFIVKGHQ	QYQSPHRFLV	
A. salmonicida		GELVSKPYID	ITLHIMNSSG	VV..IEH.DN	YKLFYIKGNQ	SIVSPGDFLV	
B. pertussis		GELISKPYIE	ITLNLMARFG	VS..V.RRDG	WRAFTIARDA	VYRGPGRMAI	
Consensus		-----	-----	-----	-----	-----	

FIG. 20F

PG2982	PGDPSSTAFP	LVAALLVEGS	DVTIRNVLMN	PTRTGL...	I	LTLQEMGADI	350
LBAA	PGDPSSTAFP	LVAALLVEGS	DVTIRNVLMN	PTRTGL...	I	LTLQEMGADI	
Agrobacterium CP4	PGDPSSTAFP	LVAALLVPGS	DVTILNVLMN	PTRTGL...	I	LTLQEMGADI	
B. subtilis	PGDISSAAFF	LAAGAMVPNS	RIVLKNVGLN	PTRTGI...	I	DVLQNMGAKL	
S. aureus	PGDISSAAFF	IYAALITPGS	DVTIHNVGIN	QIRSGI...	I	DIVEKMGGNI	
S. cerevisiae	ESDASSATYP	LAFAA.MTGT	TVTVPNIGFE	SLOGDARFAR		DVLKPMGCKI	
A. nidulans	ESDASCATYP	LAVAA.VTGT	TCTVPNIGSA	SLOGDARFAV		EVL RPMGCTV	
B. napus	EGDASSASYF	LAGAA.ITGE	TVTVEGCGTT	SLOGDVKFA.		EVLEKMGCKV	
A. thaliana	EGDASSASYF	LAGAA.ITGE	TVTVEGCGTT	SLOGDVKFA.		EVLEKMGCKV	
N. tabacum	EGDASSASYF	LAGAA.VTGG	TVTVEGCGTS	SLOGDVKFA.		EVLEKMGAEV	
L. esculentum	EGDASSASYF	LAGAA.VTGG	TVTVEGCGTS	SLOGDVKFA.		EVLEKMGAEV	
P. hybrida	EGDASSASYF	LAGAA.VTGG	TITVEGCGTN	SLOGDVKFA.		EVLEKMGAEV	
Z. mays	EGDASSASYF	LAGAA.ITGG	TVTVEGCGTT	SLOGDVKFA.		EVLEMMGAKV	
S. gallinarum	EGDASSASYF	LAAGA.IKGG	TVKVTGIGRK	SMQGDIRFA.		DVLEKMGATI	
S. typhimurium	EGDASSASYF	LAAGA.IKGG	TVKVTGIGRK	SMQGDIRFA.		DVLEKMGATI	
S. typhi	EGDASSASYF	LAAGG.IKGG	TVKVTGIGGK	SMQGDIRFA.		DVLHKMGATI	
E. coli	EGDASSASYF	LAAA.IKGG	TVKVTGIGRN	SMQGDIRFA.		DVLEKMGATI	
K. pneumoniae	EGDASSASYF	LAAGA.IKGG	TVKVTGIGRN	SVQGDIRFA.		DVLEKMGATV	
Y. enterocolitica	EGDASSASYF	LAAA.IKGG	TVRVTGIGKQ	SVQGDTKFA.		DVLEKMGAKI	
H. influenzae	EGDASSASYF	LAAGA.IK.G	KVKVTGIGKN	SIQGDRLFA.		DVLEKMGAKI	
P. multocida	EGDASSASYF	LAAA.IK.G	KVKVTGVGKN	SIQGRDLFA.		DVLEKMGAKI	
A. salmonicida	EGDASSASYF	LAAGA.IK.G	KVRVTGIGKH	SI.GDIHFA.		DVLERMGARI	
B. pertussis	EGDASTASYF	LALGA.IGGG	PVRVTGVGED	SIQGDVAFA.		ATLAAMGADV	
Consensus	---D-S---	-----	-----	-----	---	-----MG---	

FIG. 20G

PG2982	351	EVLNARLAGG	EDVADLRVR.	ASKLKGVVVP	PERAPSMIDE	YPVLAIAASF	400
LBAA		EVLNARLAGG	EDVADLRVR.	ASKLKGVVVP	PERAPSMIDE	YPVLAIAASF	
Agrobacterium CP4		EVINPRLAGG	EDVADLRVR.	SSTLKGVTVP	EDRAPSMIDE	YPILAVAAAF	
B. subtilis		EIKPSADSGA	EPYGLIIE.	TSSLKAVEIG	GDIIPRLIDE	IPIIALLATQ	
S. aureus		QL.FNQTTGA	EPTASIRIQY	TPMLQPITIE	GELVPKAIDE	LPVIALLCCTQ	
S. cerevisiae	TQTATS	TTVSGPPV..	...GTLKPLK	HVDMPEMTDA	FLTACVVAAI	
A. nidulans	EQTETS	TTVTGSPD..	...GILRATS	KRGYGT.NDR	CVPRCFRTGS	
B. napus	SWTENS	VTVTGSPSRDA	FGMRHLRAV.	DVNMNKMPDV	AMTLAVVALF	
A. thaliana	SWTENS	VTVTGPPRDA	FGMRHLRAI.	DVNMNKMPDV	AMTLAVVALF	
N. tabacum	TWTENS	VTVKGPPRNS	SGMKHLRAV.	DVNMNKMPDV	AMTLAVVALF	
L. esculentum	TWTENS	VTVKGPPRNS	SGMKHLRAI.	DVNMNKMPDV	AMTLAVVALF	
P. hybrida	TWTENS	VTVKGPPRSS	SGRKHLRAI.	DVNMNKMPDV	AMTLAVVALY	
Z. mays	TWTETS	VTVTGPPREP	FGRKHLKAI.	DVNMNKMPDV	AMTLAVVALF	
S. gallinarum	TWGDDF	I.....A	CTRGELHAI.	DMDMNHIPDA	AMTIATTALF	
S. typhimurium	TWGDDF	I.....A	CTRGELHAI.	DMDMNHIPDA	AMTIATTALF	
S. typhi	TWGDDF	I.....A	CTRGELHAI.	DMDMNHIPDA	AMTIATTALF	
E. coli	CWGDDY	I.....S	CTRGELNAI.	DMDMNHIPDA	AMTIATAALF	
K. pneumoniae	TWGEDY	I.....A	CTRGELNAI.	DMDMNHIPDA	AMTIATAALF	
Y. enterocolitica	SWGDDY	I.....E	CSRGELQGI.	DMDMNHIPDA	AMTIATTALF	
H. influenzae	TWGEDF	I.....Q	AEHAELNGI.	DMDMNHIPDA	AMTIATTALF	
P. multocida	TWGDDF	I.....Q	VEKGNLKGI.	DMDMNHIPDA	AMTIATTALF	
A. salmonicida	TWGDDF	I.....E	AEQGPLHGV.	DMDMNHIPDV	GHDHSGQSHC	
B. pertussis	RYGPGW	IETRGVRVAE	GGR..LKAF.	DADFNLIPDA	AMTAATLALY	
Consensus		-----	-----	-----	-----	-----	

FIG. 20H

PG2982	ETVMDGLDEL	RVKESDRLAA	VARGLEANGV	DCTEGEMSLT	450
LBAA	ETVMDGLDEL	RVKESDRLAA	VARGLEANGV	DCTEGEMSLT	
Agrobacterium CP4	ATVMNGLEEL	RVKESDRLSA	VANGLKLVG	DCDEGETSLV	
B. subtilis	TTVIKDAEEL	KVKETNRIDT	VVSELRLKGA	EIEPTADGMK	
S. aureus	TSTIKDAEEL	KVKETNRIDT	TADMLNLLGF	ELQPTNDGLI	
S. cerevisiae	TTTIEGIANQ	RVKECNRILA	MATELAKFGV	KTTTEL PDG IQ	
A. nidulans	PPVSSGIANQ	RVKECNRIKA	MKDELAKFGV	ICREHDDGLE	
B. napus	PTTIRDVASW	RVKETERMIA	ICTELRKLGA	TV. EEGSDYC	
A. thaliana	PTTIRDVASW	RVKETERMIA	ICTELRKLGA	TV. EEGSDYC	
N. tabacum	PTAIRDVASW	RVKETERMIA	ICTELRKLGA	TV. VEGSDYC	
L. esculentum	PTTIRDVASW	RVKETERMIA	ICTELRKLGA	TV. VEGSDYC	
P. hybrida	PTAIRDVASW	RVKETERMIA	ICTELRKLGA	TV. EEGPDYC	
Z. mays	PTAIRDVASW	RVKETERMVA	IRTELTKLGA	SV. EEGPDYC	
S. gallinarum	TTTLRNIYNW	RVKETDRLFA	MATELRKVGA	EV. EEGHDYI	
S. typhimurium	TTTLRNIYNW	RVKETDRLFA	MATELRKVGA	EV. EEGHDYI	
S. typhi	TTTLRNIYNW	RVKETDRLFA	MATELRKVGA	EV. EEGHDYI	
E. coli	TTTLRNIYNW	RVKETDRLFA	MATELRKVGA	EV. EEGHDYI	
K. pneumoniae	TTTLRNIYNW	RVKETDRLFA	MATELRKVGA	EV. EEGHDYI	
Y. enterocolitica	PTVIRNIYNW	RVKETDRLSA	MATELRKVGA	EV. EEGQDYI	
H. influenzae	ETVIRNIYNW	RVKETDRLTA	MATELRKVGA	EV. EEGEDFI	
P. multocida	ETVIRNIYNW	RVKETDRLTA	MATELRKVGA	EV. EEGEDFI	
A. salmonicida	VPPHSQHLQL	AVRD.DRCTP	CTHGHRRAQA	GVSEEGTTFI	
B. pertussis	PCRLRNIGSW	RVKETDRIHA	MHTELEKLGA	GV.QSGADWL	
Consensus	-----	-V-----R-	-----	-----	

FIG. 20I

PG2982	VRGRPDGKGL	G...	GG...	TVATHLDHRI	AMSFLVMGLA	A
LBAA	VRGRPDGKGL	G...	GG...	TVATHLDHRI	AMSFLVMGLA	A
Agrobacterium CP4	VRGRPDGKGL	GNASGA...		AVATHLDHRI	AMSFLVMGLV	S
B. subtilis	VYGKQTLKG.	...	GA...	AVSSHGDHRI	GMMLGIASCI	T
S. aureus	IHPSEFTN.	AT.....	DI..LTDHRI	GMMLAVACVL	S
S. cerevisiae	VHGLNSIKDL	KVPSDSSGPV		GVCTYDDHRV	AMSFSLLAGM	VNSQNERDEV	
A. nidulans	IDGIDR.SNL	RQPVG.....		GVFCYDDHRV	AFSFSVL.SL	VTPQ.....	
B. napus	VITP..PAKV	KPA.....		EIDTYDDHRM	AMAFSLAAC.	A
A. thaliana	VITP..PKKV	KTA.....		EIDTYDDHRM	AMAFSLAAC.	A
N. tabacum	IITP..PEKL	NVT.....		EIDTYDDHRM	AMAFSLAAC.	A
L. esculentum	IITP..PEKL	NVT.....		EIDTYDDHRM	AMAFSLAAC.	A
P. hybrida	IITP..PEKL	NVT.....		DIDTYDDHRM	AMAFSLAAC.	A
Z. mays	IITP..PEKL	NVT.....		AIDTYDDHRM	AMAFSLAAC.	A
S. gallinarum	RITP..PAKL	QHA.....		DIGTYNDHRM	AMCFSLVAL.	A
S. typhimurium	RITP..PAKL	QHA.....		DIGTYNDHRM	AMCFSLVAL.	S
S. typhi	RITP..PAKL	QHA.....		DIGTYNDHRM	AMCFSLVAL.	S
E. coli	RITP..PEKL	NFA.....		EIATYNDHRM	AMCFSLVAL.	S
K. pneumoniae	RITP..PLTL	QFA.....		EIGTYNDHRM	AMCFSLVAL.	S
Y. enterocolitica	RVVP..PAQL	IAA.....		EIGTYNDHRM	AMCFSLVAL.	S
H. influenzae	RIQPLALNQF	KHA.....		NIETYNDRM	AMCFSLIAL.	S
P. multocida	RIQPLNLAQF	QHA.....		ELNI.HDRM	AMCFALIAL.	S
A. salmonicida	TRDAADPAQA	RRD.....		R..HLQRSRI	AMCFSLVAL.	S
B. pertussis	EVAPPEPGGW	RDA.....		HIGTWDDHRM	AMCFLLAAF.	S
Consensus	-----	-----	-----	-----R-	-----	-----	-----

FIG. 20J

501	PG2982	EKPVTVDDSN	MIATSFPEFM	DMMPGLGAKI	ELSIL	538
	LBAA	EKPVTVDDSN	MIATSFPEFM	DMMPGLGAKI	ELSIL	
	Agrobacterium CP4	ENPVTVDDAT	MIATSFPEFM	DLMAGLGAKI	ELSDTKAA	
	B. subtilis	EEPIEIEHTD	AIHVSYPYTF	EHLNKLKSKS		
	S. aureus	SEPVKIKQFD	AVNVSPGFL	PKLKLQNEG		
	S. cerevisiae	ANPVRILERH	CTGKTWPGWW	DVLH		
	A. nidulans	..PTLILEKE	CVGKTWPGWW	DTLRQLFKV		
	B. napus	DVPVTIKDPG	CTRKTFPDYF	QVLESITKH		
	A. thaliana	DVPITINDSG	CTRKTFPDYF	QVLERITKH		
	N. tabacum	DVPVTIKDPG	CTRKTFPNYF	DVLQQYSKH		
	L. esculentum	DVPVTIKNPG	CTRKTFPDYF	EVLQKYSKH		
	P. hybrida	DVPVTINDPG	CTRKTFPNYF	DVLQQYSKH		
	Z. mays	EVPVTIRDPG	CTRKTFPDYF	DVLSTFVKV		
	S. gallinarum	DTPVTIILDPK	CTAKTFPDYF	EQLARMSTPA		
	S. typhimurium	DTPVTIILDPK	CTAKTFPDYF	EQLARMSTPA		
	S. typhi	DTPVTIILDPK	CTAKTFPDYF	EQLARMSTPA		
	E. coli	DTPVTIILDPK	CTAKTFPDYF	EQLARISQAA		
	K. pneumoniae	DTPVTIILDPK	CTAKTFPDYF	GQLARISTLA		
	Y. enterocolitica	DTPVTIILDPK	CTAKTFPDYF	EQLARLSQIA		
	H. influenzae	NTPVTIILDPK	CTAKTFPTFF	NEFE...KI	CLKN	
	P. multocida	KTSVTIILDPK	CTAKTFPTFL	ILFTLNTREV	AYR	
	A. salmonicida	DIAVTINDPG	CTSKTFPDYF	DKLASVSQAV		
	B. pertussis	PAAVRILDPG	CVSKTFPDYF	DVYAGLLAAR	D	
	Consensus	-----P	-----P	-----P	-----P	

FIG. 20K

TTT CGG GCC ATG GGA GCA GAA ATC AGC GAA CTA AAT TCA GAA AAA ATC	532
Phe Arg Ala Met Gly Ala Glu Ile Ser Glu Leu Asn Ser Glu Lys Ile	75 80 85
ATC GTT CAG GGT CGG GGT CTG GGA CAG TTG CAG GAA CCC AGT ACC GTT	580
Ile Val Gln Gly Arg Gly Leu Glu Gln Glu Pro Ser Thr Val	90 95 100
TTG GAT GCG GGG AAC TCT GGC ACC ACC ATG CGC TTA ATG TTG GGC TTG	628
Leu Asp Ala Gly Asn Ser Gly Thr Thr Met Arg Leu Met Leu Gly Leu	105 110 115
CTA GCC GGG CAA AAA GAT TGT TTA TTC ACC GTC ACC GGC GAT GAT TCC	676
Leu Ala Gly Gln Lys Asp Cys Leu Phe Thr Val Thr Gly Asp Ser	120 125 130
CTC CGT CAC CGC CCC ATG TCC CGG GTA ATT CAA CCC TTG CAA CAA ATG	724
Leu Arg His Arg Pro Met Ser Arg Val Ile Gln Pro Leu Gln Met	135 140 145 150
GGG GCA AAA ATT TGG GCC GCG AGT AAC GGC AAG TTT GCG CCG CTG GCA	772
Gly Ala Lys Ile Trp Ala Arg Ser Asn Gly Lys Phe Ala Pro Leu Ala	155 160 165
GTC CAG GGT AGC CAA TTA AAA CCG ATC CAT TAC CAT TCC CCC ATT GCT	820
Val Gln Gly Ser Gln Leu Lys Pro Ile His Tyr His Ser Pro Ile Ala	170 175 180

FIG. 21B

TCA GCC CAG GTA AAG TCC TGC CTG TTG CTA GCG GGG TTA ACC ACC GAG	868
Ser Ala Gln Val Lys Ser Cys Leu Leu Ala Gly Leu Thr Thr Glu	
	185
	190
	195
GGG GAC ACC ACG GTT ACA GAA CCA GCT CTA TCC CGG GAT CAT AGC GAA	916
Gly Asp Thr Thr Val Thr Glu Pro Ala Leu Ser Arg Asp His Ser Glu	
	200
	205
	210
CGC ATG TTG CAG GCC TTT GGA GCC AAA TTA ACC ATT GAT CCA GTA ACC	964
Arg Met Leu Gln Ala Phe Thr Gln Ala Lys Leu Thr Ile Asp Pro Val Thr	
	215
	220
	225
CAT AGC GTC ACT GTC CAT GGC CCG GCC CAT TTA ACG GGG CAA CGG GTG	1012
His Ser Val Thr Val His His Ala Pro Ala His Leu Thr Gly Gln Arg Val	
	235
	240
	245
GTG GTG CCA GGG GAC ATC AGC TCG GCG GCC TTT TGG TTA GTG GCG GCA	1060
Val Val Pro Gly Asp Ile Ser Ser Ala Ala Phe Trp Leu Val Ala Ala	
	250
	255
	260
TCC ATT TTG CCT GGA TCA GAA TTG TTG GTG GAA AAT GTA GGC ATT AAC	1108
Ser Ile Leu Pro Gly Ser Glu Leu Leu Val Val Glu Asn Val Gly Ile Asn	
	265
	270
	275
CCC ACC AGG ACA GGG GTG TTG GAA GTG TTG GCC CAG ATG GGG GCG GAC	1156
Pro Thr Arg Thr Gly Val Leu Glu Val Leu Ala Gln Met Gly Ala Asp	
	280
	285
	290

FIG. 21C

ATT ACC CCG GAG AAT GAA CGA TTG GTA ACG GGG GAA CCG GTA GCA GAT Ile Thr Pro Glu Asn Glu Arg Leu Val Thr Gly Glu Pro Val Ala Asp 295 300 305 310	1204
CTG CGG GTT AGG GCA AGC CAT CTC CAG GGT TGC ACC TTC GGC GGC GAA Leu Arg Val Arg Ala Ser His Leu Gln Gly Cys Thr Phe Gly Gly Glu 315 320 325	1252
ATT ATT CCC CGA CTG ATT GAT GAA ATT CCC ATT TTG GCA GTG GCG GCG Ile Ile Pro Arg Arg Leu Ile Asp Glu Ile Pro Ile Leu Ala Val Ala Ala 330 335 340	1300
GCC TTT GCA GAG GGC ACT ACC CGC ATT GAA GAT GCC GCA GAA CTG AGG Ala Phe Ala Glu Gly Thr Thr Arg Ile Glu Asp Ala Ala Glu Leu Arg 345 350 355	1348
GTT AAA GAA AGC GAT CGC CTG GCG GCC ATT GCT TCG GAG TTG GGC AAA Val Lys Glu Ser Asp Arg Leu Ala Ala Ile Ala Ser Glu Leu Gly Lys 360 365 370	1396
ATG GGG GCC AAA GTC ACC GAA TTT GAT GAT GGC CTG GAA ATT CAA GGG Met Gly Ala Lys Val Thr Glu Phe Asp Asp Gly Leu Glu Ile Gln Gly 375 380 385 390	1444
GGA AGC CCG TTA CAA GGG GCC GAG GTG GAT AGC TTG ACG GAT CAT CGC Gly Ser Pro Leu Gln Gly Ala Glu Val Asp Ser Leu Thr Asp His Arg 395 400 405	1492

FIG. 21D

ATT GCC ATG GCG TTG GCG ATC GCC GCT TTA GGT AGT GGG GGG CAA ACA Ile Ala Met Ala Leu Ala Ile Ala Ala Ala Leu Gly Ser Gly Gln Thr	1540
	410
	415
	420
ATT ATT AAC CGG GCG GAA GCG GCC GGC ATT TCC TAT CCA GAA TTT TTT Ile Ile Asn Arg Ala Glu Ala Ala Ala Ile Ser Tyr Pro Glu Phe Phe	1588
	425
	430
	435
GGC ACG CTA GGG CAA GTT GCC CAA GGA TAAAGTTAGA AAAACTCCTG Gly Thr Leu Gly Gln Val Ala Gln Gly	1635
	440
	445
GGCGGTTTGT AAATGTTTTTA CCAAGGTAGT TTGGGGTAAAGGCCCCAGCA AGTGTGCCA	1695
GGGTAATTTA TCCGCAATTG ACCAATCGGC ATGGACCGTA TCGTTCAAAC TGGGTAATTC	1755
TCCCTTTAAT TCCTTAAAG CTCGCTTAA ACTGCCCAAC GTATCTCCGT AATGGCGAGT	1815
GAGTAGAAGT AATGGGGCCA AACGGCGATC GCCACGGGAA ATTAAGCCT GCATCACTGA	1875
CCACTTATAA CTTTCGGGA	1894

FIG. 21E

TTTAAAAACA	ATGAGTTAA	AAATTATTT	TCTGGCACAC	GCGCTTTTT	TGCATTTTT	60
CTCCCATTTT	TCCGGCACAA	TAAGTTGGT	TTTATAAAG	GAAATG	ATG ATG ACG	115
				Met Met Thr		
AAT ATA TGG CAC ACC GCG CCC GTC TCT GCG CTT TCC GGC GAA ATA ACG						163
Asn Ile Trp His Thr Ala Pro Val Ser Ala Leu Ser Gly Glu Ile Thr						
ATA TGC GGC GAT AAA TCA ATG TCG CAT CGC GCC TTA TTA TTA GCA GCG						211
Ile Cys Gly Asp Lys Ser Met Ser His Arg Ala Leu Leu Ala Ala						
TTA GCA GAA GGA CAA ACG GAA ATC CGC GGC TTT TTA GCG TGC GCG GAT						259
Leu Ala Glu Gly Gln Thr Glu Ile Arg Gly Phe Leu Ala Cys Ala Asp						
TGT TTG GCG ACG CGG CAA GCA TTG CGC GCA TTA GGC GTT GAT ATT CAA						307
Cys Leu Ala Thr Arg Gln Ala Leu Arg Ala Leu Gly Val Asp Ile Gln						
AGA GAA AAA GAA ATA GTG ACG ATT CGC GGT GTG GGA TTT CTG GGT TTG						355
Arg Glu Lys Ile Val Thr Ile Arg Gly Val Gly Phe Leu Gly Leu						

FIG. 22A

CAG CCG CCG AAA GCA CCG TTA AAT ATG CAA AAC AGT GGC ACT AGC ATG Gln Pro Pro Lys Ala Pro Ile Leu Asn Met Gln Asn Ser Gly Thr Ser Met 85 90 95	403
CGT TTA TTG GCA GGA ATT TTG GCA GCG CAG CGC TTT GAG AGC GTG TTA Arg Leu Leu Ala Gly Ile Leu Ala Ala Gln Arg Phe Glu Ser Val Leu 100 105 110	451
TGC GGC GAT GAA TCA TTA GAA AAA CGT CCG ATG CAG CGC ATT ATT ACG Cys Gly Asp Glu Ser Leu Glu Lys Arg Pro Met Gln Arg Ile Ile Thr 120 125	499
CCG CTT GTG CAA ATG GGG GCA AAA ATT GTC AGT CAC AGC AAT TTT ACG Pro Leu Val Gln Met Gly Ala Lys Ile Val Ser His Ser Asn Phe Thr 135 140 145	547
GCG CCG TTA CAT ATT TCA GGA CGC CCG CTG ACC GGC ATT GAT TAC GCG Ala Pro Leu His Ile Ser Gly Arg Pro Leu Thr Gly Ile Asp Tyr Ala 150 155 160	595
TTA CCG CTT CCC AGC GCG CAA TTA AAA AGT TGC CTT ATT TTG GCA GGA Leu Pro Leu Pro Ser Ala Gln Leu Lys Ser Cys Leu Ile Leu Ala Gly 165 170 175	643
TTA TTG GCT GAC GGT ACC ACG CGG CTG CAT ACT TGC GGC ATC AGT CGC Leu Leu Ala Asp Gly Thr Thr Arg Leu His Thr Cys Gly Ile Ser Arg 180 185 190 195	691

FIG. 22B

GAC CAC ACG GAA CGC ATG TTG CCG CTT TTT GGT GGC GCA CTT GAG ATC	739
Asp His Thr Glu Arg Met Leu Pro Leu Phe Gly Gly Ala Leu Glu Ile	210
AAG AAA GAG CAA ATA ATC GTC ACC GGT GGA CAA AAA TTG CAC GGT TGC	787
Lys Lys Glu Gln Ile Ile Val Thr Gly Gln Lys Leu His Gly Cys	225
GTG CTT GAT ATT GTC GGC GAT TTG TCG GCG GCG GCG TTT TTT ATG GTT	835
Val Leu Asp Ile Val Gly Asp Leu Ser Ala Ala Ala Phe Phe Met Val	240
GCG GCT TTG ATT GCG CCG CGC GCG GAA GTC GTT ATT CGT AAT GTC GGC	883
Ala Ala Leu Ile Ala Pro Arg Ala Glu Val Ile Arg Asn Val Gly	255
ATT AAT CCG ACG CCG GCG GCA ATC ATT ACT TTG CAA AAA ATG GGC	931
Ile Asn Pro Thr Arg Ala Ile Ile Thr Leu Leu Gln Lys Met Gly	275
GGA CGG ATT GAA TTG CAT CAT CAG CGC TTT TGG GGC GCC GAA CCG GTG	979
Gly Arg Ile Glu Leu His His Thr Phe Trp Gly Ala Glu Pro Val	290
GCA GAT ATT GTT GTT TAT CAT TCA AAA TTG CGC GGC ATT ACG GTG GCG	1027
Ala Asp Ile Val Val Tyr His Ser Lys Leu Arg Gly Ile Thr Val Ala	305

FIG. 22C

CCG GAA TGG ATT GCC AAC GCG ATT GAT GAA TTG CCG ATT TTT TTT ATT	1075
Pro Glu Trp Ile Ala Asn Ala Ile Asp Glu Leu Pro Ile Phe Phe Ile	
310 315 320	
GCG GCA GCT TGC GCG GAA GGG ACG ACT TTT GTG GGC AAT TTG TCA GAA	1123
Ala Ala Cys Ala Glu Gly Thr Thr Phe Val Gly Asn Leu Ser Glu	
325 330 335	
TTG CGT GTG AAA GAA TCG GAT CGT TTA GCG GCG ATG GCG CAA AAT TTA	1171
Leu Arg Val Lys Glu Ser Asp Arg Leu Ala Ala Met Ala Gln Asn Leu	
340 345 350 355	
CAA ACT TTG GCG GTG GCG TGC GAC GTT GGC GCC GAT TTT ATT CAT ATA	1219
Gln Thr Leu Gly Val Ala Cys Asp Val Gly Ala Ala Asp Phe Ile His Ile	
360 365 370	
TAT GGA AGA AGC GAT CGG CAA TTT TTA CCG GCG CGG GTG AAC AGT TTT	1267
Tyr Gly Arg Ser Asp Arg Gln Phe Leu Pro Ala Arg Val Asn Ser Phe	
375 380 385	
GGC GAT CAT CCG ATT GCG ATG AGT TTG GCG GTG GCA GGT GTG CGC GCG	1315
Gly Asp His Arg Ile Ala Met Ser Leu Ala Val Ala Gly Val Arg Ala	
390 395 400 405	
GCA GGT GAA TTA TTG ATT GAT GAC GCG GTG GCG GCG GGT TCT ATG	1363
Ala Gly Glu Leu Ile Asp Gly Ala Val Ala Ala Val Ser Met	
405 410 415	

FIG. 22D

CCG CAA TTT CGC GAT TTT GCC GCC GCA ATT GGT ATG AAT GTA GGA GAA	1411
Pro Gln Phe Arg Asp Phe Ala Ala Ile Gly Met Asn Val Gly Glu	
420 425 430 435	
AAA GAT GCG AAA AAT TGT CAC GAT TGATGGTCCT AGCGGTGTTG GAAAAGGCAC	1465
Lys Asp Ala Lys Asn Cys His Asp	
440	
GGTGGCGCAA GCTT	1479

FIG. 22E

FIG. 23A

1	PG2982	MS	HSASPKPATA	RRSEALTGEI	RIPGDKSISH	40
	LBAA	MS	HSASPKPATA	RRSEALTGEI	RIPGDKSISH	
	Agrobacterium CP4	MS	HGASSRPATA	RKSSGLSGTV	RIPGDKSISH	
	Synechocystis sp. PCC6803		MALLSLNNHQ	SHQRLTVNPP	RVPGDKSISH	
	B. subtilis			MR	HIPGDKSISH	
	D. nodosus			MMTNiWHT	TICGDKSMSh	
	S. aureus			MVNEQII	EVPGDKSMTH	
	Consensus				<u>I-GDKS</u> --H	

41	PG2982	RSFMFGGLAS	GETRITGLLE	GEDVINTGRA	MQAMGAKI.R	80
	LBAA	RSFMFGGLAS	GETRITGLLE	GEDVINTGRA	MQAMGAKI.R	
	Agrobacterium CP4	RSFMFGGLAS	GETRITGLLE	GEDVINTGKA	MQAMGARI.R	
	Synechocystis sp. PCC6803	RALMLGAIAT	GETIIEGLLL	GEDPRSTAHc	FRAMGAEISE	
	B. subtilis	RSVMFGALAA	GTTTVKNFLP	GADCLSTIDC	FRKMGVHI.E	
	D. nodosus	RALLLAALAE	GQTEIRGFLA	CADCLATRQA	LRALGVDI.Q	
	S. aureus	RAIMLASLAE	GVSTIYKPLL	GEDCRRTMdI	FRHLGVEI.K	
	Consensus	R--MF---A-	G---I---L-	--D---T---	---MG--I--	

81	PG2982	KEGDVWIING	VNGGCLLQPE	AALDFGNAGT	GARLTMGLVG	120
	LBAA	KEGDVWIING	VNGGCLLQPE	AALDFGNAGT	GARLTMGLVG	
	Agrobacterium CP4	KEGDTWIIDG	VNGGGLLAPE	APLDFGNAAT	GCRLTMGLVG	
	Synechocystis sp. PCC6803	LNSEKIIVQG	RGLGQLQEPS	TVLDAGNSGT	TMRLMLGLLA	
	B. subtilis	QSSSDVVIHG	KGIDALKEPE	SLLDVGNsGT	TIRLMGILA	
	D. nodosus	REKEIVTIRG	VGFLGLOPPK	APLNMQNSGT	SMRLLAGILA	
	S. aureus	EDDEKLVVTS	PGYQ.VNTPH	QVLYTGNsGT	TTRLLAGLLS	
	Consensus	-----I--	-G-----P-	--L---N--T	--RL--G---	

FIG. 23B

PG2982	121	TY.DMKTSFI	GDASLSKRPM	GRVLNPLRM	GVQVEAADGD	160
LBAA		TY.DMKTSFI	GDASLSKRPM	GRVLNPLRM	GVQVEAADGD	
Agrobacterium CP4		VY.DFDSTFI	GDASLTKRPM	GRVLNPLRM	GVQVKSEDDG	
Synechocystis sp. PCC6803		GQKDCCLFTVT	GDDSLRHRPM	SRVIQPLQQM	GAKIWARSNQ	
B. subtilis		G.RPFYSAVA	GDESIKRPM	KRVTEPLKKM	GAKIDGRAGG	
D. nodosus		AQR.FESVLC	GDESLEKRPM	QRIITPLVQM	GAKIVSHSNF	
S. aureus		GLGN.ESVLS	GDVSIGKRPM	DRVLRPLKLM	DANIEGIEDN	
Consensus		-----	GD-S---RPM	-RV--PL--M	---I-----	

PG2982	161	RMPLTLIGPK	TANPITYRVP	MASQVKSAV	LLAGLNTPGV	200
LBAA		RMPLTLIGPK	TANPITYRVP	MASQVKSAV	LLAGLNTPGV	
Agrobacterium CP4		RLPVTLRGPK	TPTPITYRVP	MASQVKSAV	LLAGLNTPGI	
Synechocystis sp. PCC6803		KFAPLAVQGS	QLKPIHYHSP	IASAQVKSCS	LLAGLTTEGD	
B. subtilis		EFTPLSVSGA	SLKGIDYVSP	VASAQIKSAV	LLAGLQAEGT	
D. nodosus		T.APLHISGR	PLTGIDYALP	LPSAQLKSCL	ILAGLLADGT	
S. aureus		.YTPLIIKPS	VIKGINYQME	VASAQVKSAI	LFASLFSKEP	
Consensus		-----	----I-Y----	--SAQ-KS--	-LA-L-----	

PG2982	201	TTVIEPVMTR	DHTEKMLQGF	GADLT	VETDKDGVRRH	240
LBAA		TTVIEPVMTR	DHTEKMLQGF	GADLT	VETDKDGVRRH	
Agrobacterium CP4		TTVIEPIIMTR	DHTEKMLQGF	GANLT	VETDADGVRT	
Synechocystis sp. PCC6803		TTVTEPALSR	DHSERMLQAF	GAKLT	IDPVTHSV..	
B. subtilis		TTVTEPHKSR	DHTERMLSAF	GVKLS	EDQT..SV..	
D. nodosus		TRLHTCGISR	DHTERMLPLF	GGALE	IKK..EQI..	
S. aureus		TIIEKELDVSR	NHTETMFKHF	NIPIEAEGLS	INTTPEAIRY	
Consensus		T-----R	-H-E-ML--F	-----	-L-	-----V--	

FIG. 23C

241
IRITGQGKLV GQTIDVPGDP 280
IRITGQGKLV GQTIDVPGDP SSTAFLVAA LLVEGSDVTI
IRLEGRGKLT GQVIDVPGDP SSTAFLVAA LLVEGSDVTI
.TVHGPAHLT GQRVVVPGDI SSAFWLVA SILPGSELLV
.SIAGGQKLT AADIFVPGDI SSAFFLAAG AMVPNSRIVL
.IVTGGQKLH GCVLDIVGDL SAAFFMVA LIAPRAEVI
IKPAD..... FHVPGDI SAAFFIVAA LITPGSDVTI
----- S--AF-----

PG2982
LBAA
Agrobacterium CP4
Synechocystis sp. PCC6803
B. subtilis
D. nodosus
S. aureus
Consensus

281
RNVLMNPTRT GLILTLQEMG 320
RNVLMNPTRT GLILTLQEMG ADIEVLNARL AGGEDVADLR
LNVLMNPTRT GLILTLQEMG ADIEVLNARL AGGEDVADLR
ENVGINPTRT GVLEVLAQMG ADITPENERL VTGEPVADLR
KNVGLNPTRT GIIDVLQNMG AKLEIKPSAD SGAEPYGDLI
RNVGINPTRA AIITLLQKMG GRIELHHQRF WGAEPVADIV
HNVGINQTRS GIIDIVEKMG GNIQLFNQT. TGAEPTASIR
-NV--N-TR- ----E-----

PG2982
LBAA
Agrobacterium CP4
Synechocystis sp. PCC6803
B. subtilis
D. nodosus
S. aureus
Consensus

321
VR.ASKLKG VPPERAPSM 360
VR.ASKLKG VPPERAPSM IDEYPLVLA ASFAEGETVM
VR.SSTLKG TVPEDRAPSM IDEYPLVLA ASFAEGETVM
VR.ASHLQGC TFGGEIIPRL IDEIPIILAVA AFAEGTTRI
IE.TSSLKAV EIGGDIIPRL IDEIPIALL ATQAEGETTVI
VY.HSKLRGI TVAPEWIANA IDELPIFFIA AACAEGETTFV
IQYTPMLQPI TIEGELVPKA IDELPVIAL CTQAVGTSTI
V-----L--- ----E----- IDE-PI---- -A-G----

PG2982
LBAA
Agrobacterium CP4
Synechocystis sp. PCC6803
B. subtilis
D. nodosus
S. aureus
Consensus

FIG. 23D

PG2982	361	DGLDELRVKE	SDRLAAVARG	LEANGVDCTE	GEMSLTVRGR	400
LBAA		DGLDELRVKE	SDRLAAVARG	LEANGVDCTE	GEMSLTVRGR	
Agrobacterium CP4		NGLEELRVKE	SDRLSAVANG	LKLNQVDCDE	GETSLVVRGR	
Synechocystis sp. PCC6803		EDAAELRVKE	SDRLAAIASE	LKMGAKVTE	FDDGLEIQGG	
B. subtilis		KDAAELRVKE	TNRIDTVSE	LRKLGAIEIP	TADGMKVYVK	
D. nodosus		GNLSELRVKE	SDRLAAMAQN	LQTLGVACDV	GADFIHIYGR	
S. aureus		KDAEELRVKE	TNRIDTTADM	LNLGFEHQ	TNDGLIIHPS	
Consensus		---EL-VKE	--R-----	L---G----	-----V----	

PG2982	401	PDGKGLG...	GGTVATHLDH	RIAMSFLVMG	LAAEKPVTVD	440
LBAA		PDGKGLG...	GGTVATHLDH	RIAMSFLVMG	LAAEKPVTVD	
Agrobacterium CP4		PDGKGLGNAS	GAAVATHLDH	RIAMSFLVMG	LVSENPVTVD	
Synechocystis sp. PCC6803		SPLQ.....	GAEVDSLTDH	RIAMALIAAA	LGSGGQTIIN	
B. subtilis		QTLK.G....	GAAVSSHGDH	RIGMMLGAS	CITEEPIEIE	
D. nodosus		SDRQFL....	PARVNSFGDH	RIAMSLAVAG	VRAAGELLID	
S. aureus		E.....FK	TNATDILTTH	RIGMMLAVAC	VLSSEPVKIK	
Consensus		-----	-----DH	RI-M-L-V--	-----I--	

PG2982	441	DSNMIATSFP	EFMDMPGLG	AKIELSIL..	...	437
LBAA		DSNMIATSFP	EFMDMPGLG	AKIELSIL..	...	
Agrobacterium CP4		DATMIATSFP	EFMDLMAGLG	AKIELSDTKA	A..	
Synechocystis sp. PCC6803		RAEAAAISYP	EFFGTLGQVA	QG*	...	
B. subtilis		HTDAIHVSYP	TFFEHLNKL	KKS	
D. nodosus		DGAVAASVMP	QFRDFAAIG	MNVGEKDAKN	CHD	
S. aureus		QFDVAVNSFP	GFLPKLKLQ	NEG	...	
Consensus		-----S-P	-F-----	-----	-----	

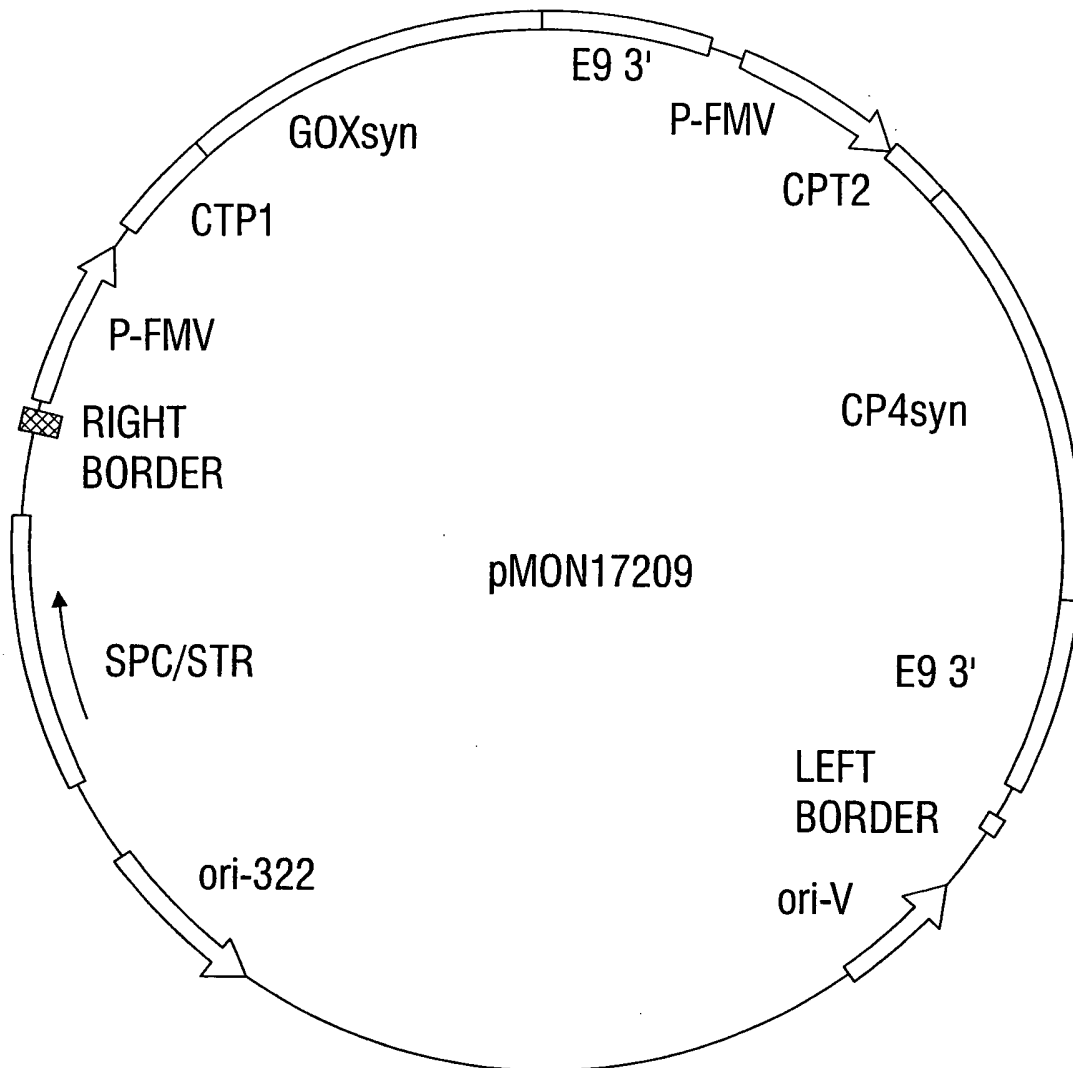


FIG. 24

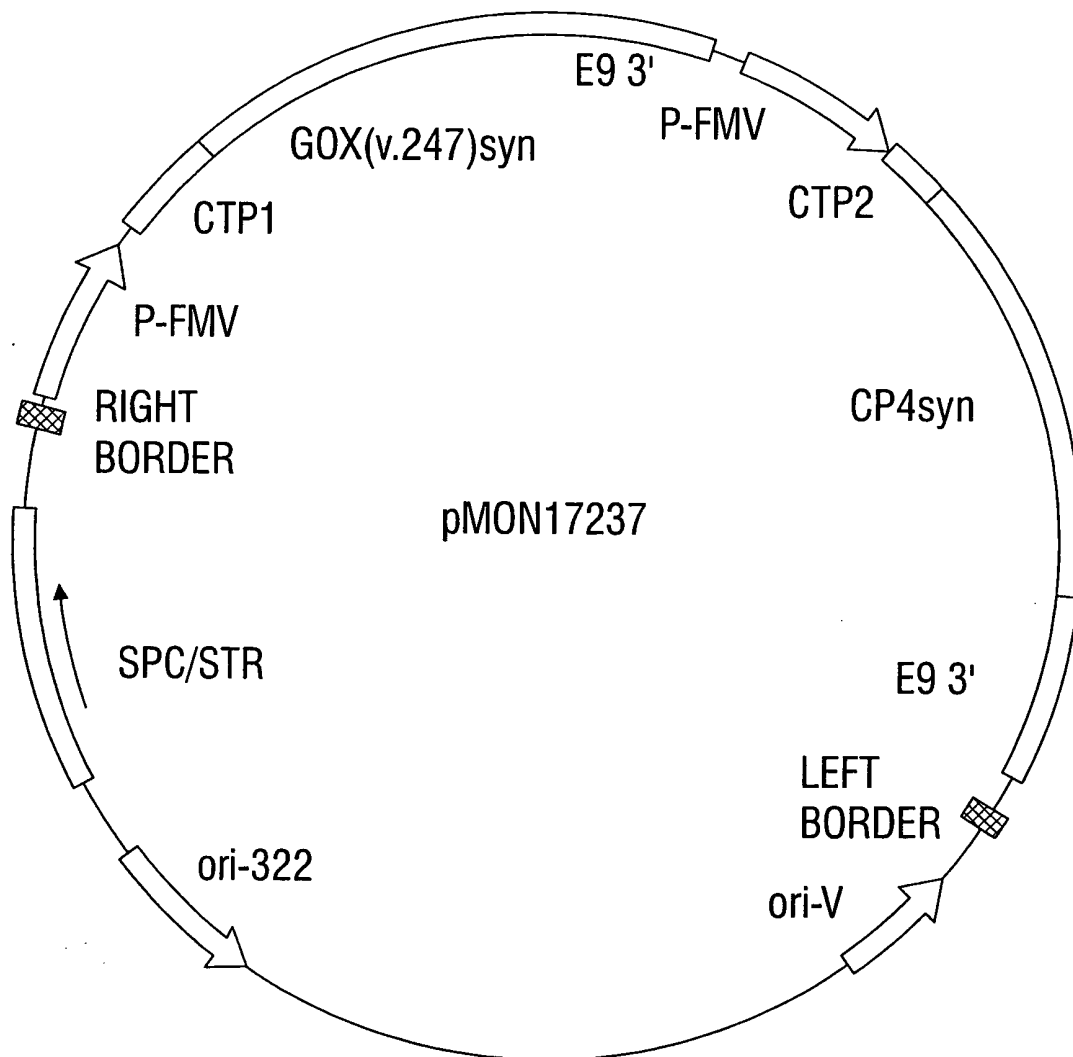


FIG. 25